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200  
↙

Sequence	Length	Code
VLAEAMSQV (SEQ ID NO:70)	9	A
ILKEPVHGV (SEQ ID NO:71)	9	B
TLNFPISPI (SEQ ID NO:72)	9	C
SLLNATDIAV (SEQ ID NO:73)	10	D
QMAVFIHNFK (SEQ ID NO:74)	10	E
VTVYYGVPVWK (SEQ ID NO:75)	11	F
FPVRPQVPL (SEQ ID NO:76)	9	G
YPLASLRSLF (SEQ ID NO:77)	10	H
VIYQYMDDLY (SEQ ID NO:78)	10	I
IYQEPFKNL (SEQ ID NO:79)	9	J
IWGCSGKLI (SEQ ID NO:80)	9	K

202

AA	C+1 ranking	N-1 ranking
K	2.20	0.64
C	2.00	1.00
N	2.00	0.00
G	1.80	1.33
T	1.50	0.00
A	1.33	1.21
F	1.33	1.00
S	1.33	0.00
W	1.20	0.00
Q	1.20	0.00
R	1.17	1.57
M	1.00	0.00
Y	1.00	0.75
I	0.86	0.50
L	0.75	2.20
V	0.00	1.19
D	0.00	0.00
H	0.00	0.00
E	0.00	0.00
P	0.00	0.00

204

Motif Specification

XXXX(FY)XX(LIMV) (SEQ ID NO:370)  
 XXXX(FY)XXX(LIMV) (SEQ ID NO:371)  
 XXXXNXXX(LIMV) (SEQ ID NO:372)  
 XXXXNXXXX(LIMV) (SEQ ID NO:373)  
 X(LM)XXXXXXXV (SEQ ID NO:374)  
 X(LM)XXXXXXXV (SEQ ID NO:375)  
 X(LMVT)XXXXXXX(KRY) (SEQ ID NO:376)  
 X(LMVT)XXXXXXX(KRY) (SEQ ID NO:377)  
 XPXXXXXXX(LIMVF) (SEQ ID NO:378)  
 XPXXXXXXX(LIMVF) (SEQ ID NO:379)

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FIG. 11A



## Replacement Sheet

Junctional Analyzer run on Saturday, February 26, 2000 09:06:23 pm.

The following non-zero AA weights will be used.

AA	N-1 ranking	C+1 ranking
A	1.21	1.33
C	1.00	2.00
F	1.00	1.33
G	1.33	1.80
I	0.50	0.86
K	0.64	2.20
L	2.20	0.75
M	0.00	1.00
N	0.00	2.00
Q	0.00	1.20
R	1.57	1.17
S	0.00	1.33
T	0.00	1.50
V	1.19	0.00
W	0.00	1.20
Y	0.75	1.00

204

The following 10 motif specifications will be used to search for junctionals.

Count	Motif Specification
1	XXXX(FY)XX(LIMV) (SEQ ID NO:370)
2	XXXX(FY)XXX(LIMV) (SEQ ID NO:371)
3	XXXXNXXX(LIMV) (SEQ ID NO:372)
4	XXXXNXXXX(LIMV) (SEQ ID NO:373)
5	X(LM)XXXXXXV (SEQ ID NO:374)
6	X(LM)XXXXXXXV (SEQ ID NO:375)
7	X(LMVT)XXXXXX(KRY) (SEQ ID NO:376)
8	X(LMVT)XXXXXX(KRY) (SEQ ID NO:377)
9	XPXXXXXX(LIMVF) (SEQ ID NO:378)
10	XPXXXXXX(LIMVF) (SEQ ID NO:379)

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Code	Peptide	Length
A	VLAEMSQV (SEQ ID NO:70)	9
B	ILKEPVHGV (SEQ ID NO:71)	9
C	TLNFPISPI (SEQ ID NO:72)	9
D	SLLNATDIAV (SEQ ID NO:73)	10
E	QMAVFIHNFK (SEQ ID NO:74)	10
F	VTVYYGVPVWK (SEQ ID NO:75)	11
G	FPVRPQVPL (SEQ ID NO:76)	9
H	YPLASLRSLF (SEQ ID NO:77)	10
I	VIYQYMDDL Y (SEQ ID NO:78)	10
J	IYQEPFKNL (SEQ ID NO:79)	9
K	IWGCSGKLI (SEQ ID NO:80)	9

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MaxInsertions = 4 (208)

FIG. 13A

## Replacement Sheet



Protein	Sequence	Restriction	(SEQ ID NO:)
HIV gag 386	VLAEAMSQV	HLA-A2	143
HIV gag 271	MTNNPPIPV	HLA-A2	144
HIV pol 774	MASDFNLPPV	HLA-A2	145
HIV pol 448	KLVGKLNWA	HLA-A2	146
HIV pol 163	LVGPTPVNI	HLA-A2	147
HIV pol 498	ILKEPVHGV	HLA-A2	148
HIV pol 879	KAACWWAGI	HLA-A2	149
HIV pol 132	KMIGGIGGFI	HLA-A2	150
HIV pol 772	RAMASDFNL	HLA-A2	151
HIV pol 183	TLNFPISPI	HLA-A2	152
HIV env 134	KLTPLCVTL	HLA-A2	153
HIV env 651	LLQLTVWGI	HLA-A2	154
HIV env 163	SLLNATDIAV	HLA-A2	155
HIV nef 221	LTFGWCFKL	HLA-A2	156
HIV vpr 59	AIIRILQQL	HLA-A2	157
HIV vpr 62	RILQQLFI	HLA-A2	158
HIV pol 929	QMAVFIHNFK	HLA-A3	159
HIV pol 722	KVYLAWVPAHK	HLA-A3	160
HIV pol 971	KIQNFRVYYR	HLA-A3	161
HIV pol 347	AIFQSSMTK	HLA-A3	162
HIV pol 98	VTIKIGGQLK	HLA-A3	163
HIV env 61	TTLFCASDAK	HLA-A3	164
HIV env 47	VTVYYGVPVWK	HLA-A3	165
HIV nef 100	QVPLRPMTYK	HLA-A3	166
HIV vif 7	VMIVWQVDR	HLA-A3	167
HIV gag 162	QMVHQAISPR	HLA-A3	168
HIV gag 545	YPLASLRSLF	HLA-B7	169
HIV gag 237	HPVHAGPIA	HLA-B7	170
HIV pol 186	FPISPIETV	HLA-B7	171
HIV pol 893	IPYNPQSQGVV	HLA-B7	172
HIV env 259	IPIHYCAPA	HLA-B7	173
HIV env 250	CPKVSFEPI	HLA-B7	174
HIV nef 94	FPVRPQVPL	HLA-B7	175
HIV rev 75	VPLQLPPL	HLA-B7	176
HIV pol 684	EVNIVTDSQY	HLA-A1	177
HIV gag 317	FRDYVDRFY	HLA-A1	178
HIV pol 368	VIYQYMDDL	HLA-A1	179
HIV pol 295	VTVLDVGDAY	HLA-A1	180
HIV pol 533	IYQEPFKNL	HLA-A24	181
HIV pol 244	PYNTPVFAI	HLA-A24	182
HIV pol 530	TYQIYQEPF	HLA-A24	183
HIV pol 597	YWQATWIPEW	HLA-A24	184
HIV env 681	IWGCSGKLI	HLA-A24	185
HIV env 671	RYLKDQQLL	HLA-A24	186

FIG. 19A

## Replacement Sheet



Protein	Sequence	Restriction	(SEQ ID NO:)
HIV env 55	VWKEATTTLF	HLA-A24	187
HIV vpr 46	IYETYGDTW	HLA-A24	188
HIV vpr 14	PYNEWTLEL	HLA-A24	189
HIV gag 298	KRWIILGLNKIVRMY	HLA-DR	190
HIV pol 596	WEFVNTPLVLKLYWYQ	HLA-DR	191
HIV pol 956	QKQITKIQNFRVYYR	HLA-DR	192
HIV pol 712	KVYLA WVP AHKGIGG	HLA-DR	193
HIV gag 294	GEIYKRWIILGLNKI	HLA-DR	194
HIV pol 711	EKVYLA WVP AHKGIGG	HLA-DR	195
HIV env 729	QHLLQLTVWGKQLQ	HLA-DR	196
HIV gag 171	QGQMVHQAI SPRTL N	HLA-DR	197
HIV pol 335	SPAIFQSSMTKILEP	HLA-DR	198
HIV env 566	IKQFINMWQEVGKAMY	HLA-DR	199
HIV pol 303	FRKYTAFTIPSINNE	HLA-DR	200
HIV pol 758	HSNWRAMASDFNLPP	HLA-DR	201
HIV pol 915	KTAVQMAVFIHNFKR	HLA-DR	202
HIV vpu 31	YRKILRQRKIDRLID	HLA-DR3	203
HIV pol 874	WAGIKQEF GIPYNPQ	HLA-DR3	204
HIV pol 674	EVNIVTDSQYALGII	HLA-DR3	205
HIV pol 619	AETFYVDGAANRETK	HLA-DR3	206
HIV pol 989	GAVVIQD NSDIK VVP	HLA-DR3	207
HCV NS4 1812	LLFNILGGWV	HLA-A2	208
HCV NS1/E2 728	FLLLADARV	HLA-A2	209
HCV NS4 1590	YLVAYQATV	HLA-A2	210
HCV NS5 2611	RLIVFPDLGV	HLA-A2	211
HCV CORE 132	DLMGYIPLV	HLA-A2	212
HCV NS4 1920	WMNRLIAFA	HLA-A2	213
HCV NS4 1666	VLVGGVLAA	HLA-A2	214
HCV NS4 1769	HMWNFISGI	HLA-A2	215
HCV NS4 1851	ILAGYGAGV	HLA-A2	216
HCV CORE 35	YLLPRRG PRL	HLA-A2	217
HCV NS1/E2 726	LLFLLLADA	HLA-A2	218
HCV LORF 1131	YLVTRHADV	HLA-A2	219
HCV CORE 51	KT SERSQPR	HLA-A3	220
HCV CORE 43	RLGVRATRK	HLA-A3	221
HCV ENV1 290	QLFTFSRR	HLA-A3	222
HCV NS1/E2 632	RMVYVG GVEHR	HLA-A3	223
HCV NS3 1396	LIFCHSKKK	HLA-A3	224
HCV NS4 1863	GVAGALVAFK	HLA-A3	225
HCV NS4 1864	VAGALVAFK	HLA-A3	226
HCV NS3 1262	LGFGAYMSK	HLA-A3	227
HCV Core 169	LPGCSFSIF	HLA-B7	228
HCV NS5 2922	LSAFSLHSY	HLA-A1	229
HCV NS3 1128	CTCGSSDLY	HLA-A1	230
HCV NS5 2180	LTDPSHITA	HLA-A1	231

FIG. 19B

# Replacement Sheet



Protein	Sequence	Restriction	(SEQ ID NO:)
HCV Core 126	LTCGFADLMGY	HLA-A1	232
HCV NS3 1305	LADGGCSGGAY	HLA-A1	233
HCV NS4 1765	FWAKHMWNF	HLA-A24	234
HCV NS5 2875	RMILMTHFF	HLA-A24	235
HCV NS5 2639	VMGSSYGF	HLA-A24	236
HCV NS4 1765	FWAKHMWNFI	HLA-A24	237
P. falciparum SSP2-230	FMKAVCDEV	HLA-A2	238
P. falciparum EXP1-83	GLLGVVSTV	HLA-A2	239
P. falciparum CSP-7	ILSVSSFLFV	HLA-A2	240
P. falciparum LSA1-94	QTNFKSLLR	HLA-A3	241
P. falciparum LSA1-105	GVSENIFLK	HLA-A3	242
P. falciparum SSP2-522	LLACAGLAYK	HLA-A3	243
P. falciparum SSP2-539	TPYAGEPAPF	HLA-B7	244
P. falciparum LSA1-1663	LPSENERGY	HLA-A1	245
P. falciparum EXP1-73	KYKLATSVL	HLA-A24	246
P. falciparum CSP-12	SFLFVEALF	HLA-A24	247
P. falciparum LSA1-10	YFILVNLLI	HLA-A24	248
P. falciparum SSP2-14	FLIFFDLFLV	HLA-A2	249
P. falciparum EXP1-80	VLAGLLGVV	HLA-A2	250
P. falciparum EXP1-91	VLLGGVGLVL	HLA-A2	251
P. falciparum SSP2-523	LACAGLAYK	HLA-A3	252
P. falciparum EXP1-10	ALFFIIFNK	HLA-A3	253
P. falciparum LSA1-11	FILVNLLIFH	HLA-A3	254
P. falciparum SSP2-126	LPYGRTNL	HLA-B7	255
P. falciparum CSP-15	FVEALFQEY	HLA-A1	256
P. falciparum LSA1-1794	FQDEENIGIY	HLA-A1	257
P. falciparum LSA1-9	FYFILVNLL	HLA-A24	258
P. falciparum SSP2-8	KYLVIVFLI	HLA-A24	259
P. falciparum CSP-394	GLIMVLSFL	HLA-A2	260
P. falciparum EXP1-2	KILSVFFLA	HLA-A2	261
P. falciparum CSP-344	VTGNGIQVR	HLA-A3	262
P. falciparum LSA1-59	HVLSHNSYEK	HLA-A3	263
P. falciparum SSP2-207	PSDGKCNLY	HLA-A1	264
P. falciparum LSA1-1671	YYIPHQSSL	HLA-A24	265
P. falciparum LSA1-1876	KFIKSLFHIF	HLA-A24	266
P. falciparum SSP2-13	VFLIFFDLFL	HLA-A24	267
P. falciparum LSA1-1881	LFHIFDGDNEI	HLA-A24	268
P. falciparum CSP-55	YYGKQENWYSL	HLA-A24	269
P. falciparum LSA1-5	LYISFYFI	HLA-A24	270
P. falciparum CSP-2	MRKLAILSVSSFLFV	HLA-DR	271
P. falciparum CSP-53	MNYYGKQENWYSLKK	HLA-DR	272
P. falciparum CSP-375	SSVFNVVNSSIGLIM	HLA-DR	273
P. falciparum SSP2-61	RHNWVNHAVPLAMKLI	HLA-DR	274
P. falciparum SSP2-165	PDSIQDSLKESRKLN	HLA-DR3	275
P. falciparum SSP2-211	KCNLYADSAWENVKN	HLA-DR3	276

FIG. 19C

## Replacement Sheet



Protein	Sequence	Restriction	(SEQ ID NO:)
P. falciparum SSP2-223	VKNVIGPFMKAVCVE	HLA-DR	277
P. falciparum SSP2-509	KYKIAGGIAGGLALL	HLA-DR	278
P. falciparum SSP2-527	GLAYKFVVPGAATPY	HLA-DR	279
P. falciparum EXP1-71	KSKYKLATSVLAGLL	HLA-DR	280
P. falciparum EXP1-82	AGLLGNVSTVLLGGV	HLA-DR	281
P. falciparum LSA1-16	LLIFHINGKIIKNSE	HLA-DR	282
P. falciparum LSA1-94	QTNFKSLLRNLGVSE	HLA-DR	283
HBV core 18	FLPSDFFPSV	HLA-A2	284
HBV env 183	FLLTRILTI	HLA-A2	285
HBV env 335	WLSLLVPFV	HLA-A2	286
HBV pol 455	GLSRYVARL	HLA-A2	287
HBV pol 538	YMDDVVLGV	HLA-A2/A1	288
HBV pol 773	ILRGTSFVYV	HLA-A2	289
HBV pol 562	FLLSLGIHL	HLA-A2	290
HBV pol 642	ALMPYACI	HLA-A2	291
HBV env 338	GLSPTVWLSV	HLA-A2	292
HBV core 141	STLPETTIVRR	HLA-A3	293
HBV pol 149	HTLWKAGILYK	HLA-A3/A1	294
HBV pol 150	TLWKAGILYK	HLA-A3	295
HBV pol 388	LVVDFSQFSR	HLA-A3	296
HBV pol 47	NVSIPWTHK	HLA-A3	297
HBV pol 531	SAICSVVRR	HLA-A3	298
HBV pol 629	KVGNTGLY	HLA-A3/A1	299
HBV pol 665	QAFTFSPTYK	HLA-A3	300
HBV core 19	LPDFFPSV	HLA-B7	301
HBV env 313	IPSSWAF	HLA-B7	302
HBV pol 354	TPARVTGGVF	HLA-B7	303
TB	RMSRVTTFTV	HLA-A2	304
TB	ALVLLMLPVV	HLA-A2	305
TB	LMIGTAAAVV	HLA-A2	306
TB	ALVLLMLPV	HLA-A2	307
TB	GLMTAVYLV	HLA-A2	308
TB	MALLRLPV	HLA-A2	309
TB	RMFAANLGV	HLA-A2	310
TB	SLYFGGICV	HLA-A2	311
TB	RLPLVLPV	HLA-A2	312
TB	RLMIGTAAA	HLA-A2	313
TB	FVVALIPLV	HLA-A2	314
TB	MTYAAPLFV	HLA-A2	315
TB	AMALLRLPLV	HLA-A2	316
p53 139	KLCPVQLWV	HLA-A2	317
CEA 687	ATVGIMIGV	HLA-A2	318
CEA 691	IMIGHLVGV	HLA-A2	319
Her2/neu 689	RLLQETELV	HLA-A2	320
MAGE3 112	KVAEIVHFL	HLA-A2	321

FIG. 19D



Protein	Sequence	Restriction	(SEQ ID NO:)
Her2/neu 369	KVFGSLAFV	HLA-A2	322
CEA 605	YLSGANLNV	HLA-A2	323
MAGE2 157	YLQLVFGIEV	HLA-A2	324
Her2/neu 665	VVLGVVFGI	HLA-A2	325
p53 149	SMPPPGRV	HLA-A2	326
PAP.21.T2	LTFFWLDRSV	HLA-A2	327
PAP.112	TLMSAMTNL	HLA-A2	328
PAP.284	IMYSAHDTTV	HLA-A2	329
PSM.288.V10	GLPSIPVHPV	HLA-A2	330
PSM.441	LLQERGVAYI	HLA-A2	331
PSM.469L2	LLYSLVHNL	HLA-A2	332
PSM.663	MMNDQLMFL	HLA-A2	333
PSA.3.V11	FLTLSVTWIGV	HLA-A2	334
PSA.143.V8	ALGTTCYV	HLA-A2	335
PSA.161	FLTPKKLQCV	HLA-A2	336
HuK2.4.L2	LLLSIALSV	HLA-A2	337
HuK2.53.V11	VLVHPQWVLTV	HLA-A2	338
HuK2.165	FLRPRSLQCV	HLA-A2	339
HuK2.216.V11	PLVCNGVLQGV	HLA-A2	340

FIG. 19E



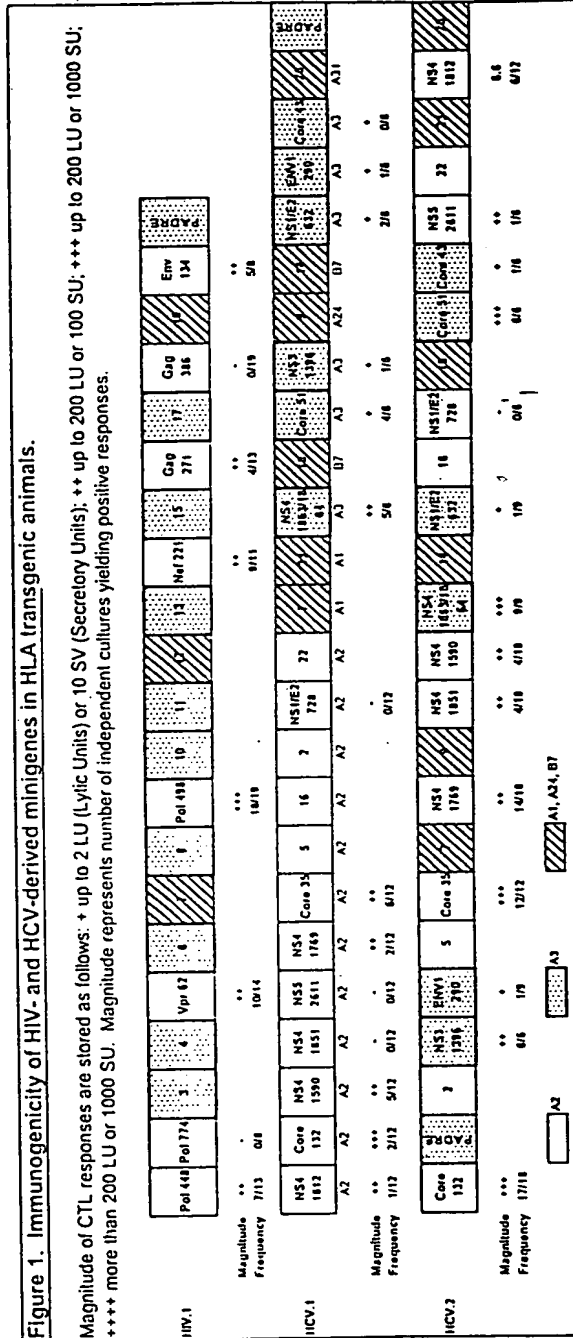
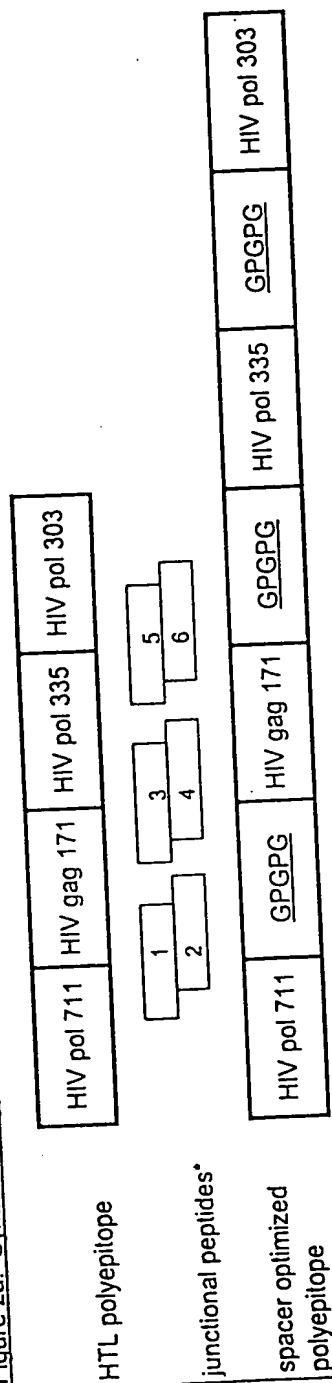


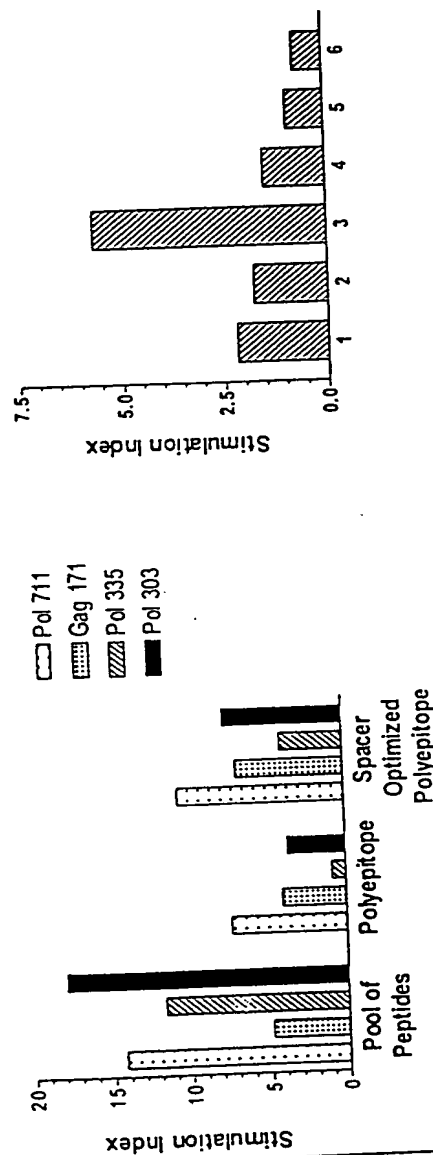
FIGURE 1

Figure 2a. Synthetic polypeptides encoding HIV-derived HTL epitopes



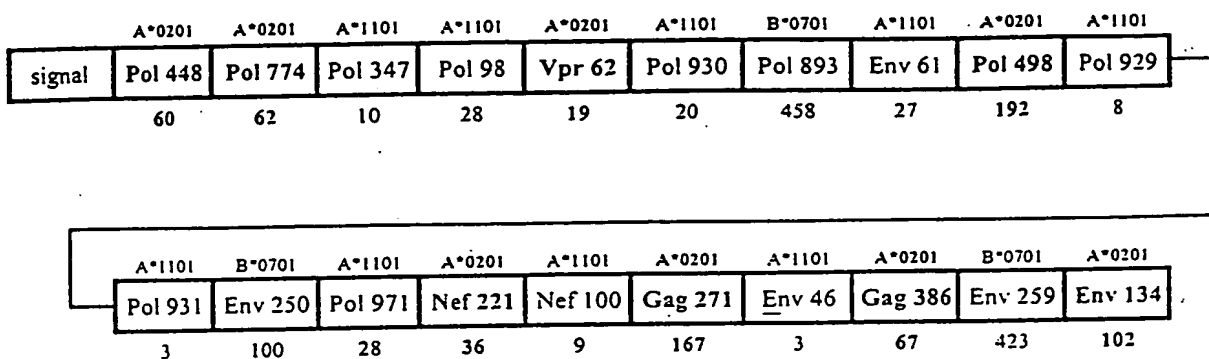
\* junctional peptides comprise either 10 amino acids from the N-terminal epitope and 5 amino acids from the C-terminal epitope or 5 amino acids from the N-terminal epitope and 10 amino acids from the C-terminal epitope.

Figure 2b. Proliferative responses to synthetic polypeptides encoding HIV-derived HTL



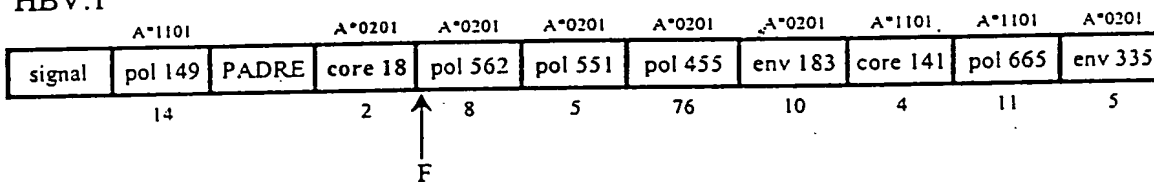


a: HIV-FT

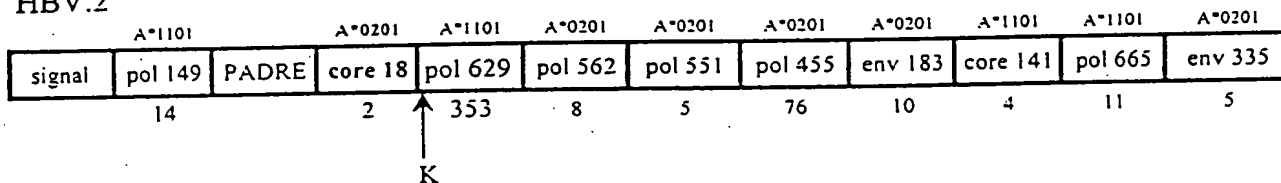


b: HBV-specific multiepitope constructs

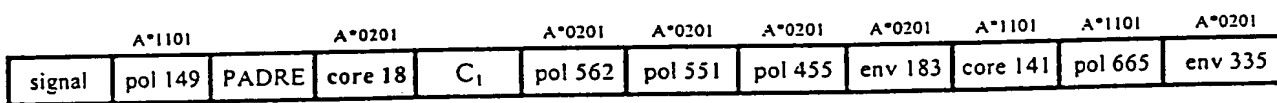
HBV.1



HBV.2



HBV.1X



C<sub>1</sub>= either W, Y, L, K, R, C, N or G

FIGURE 3

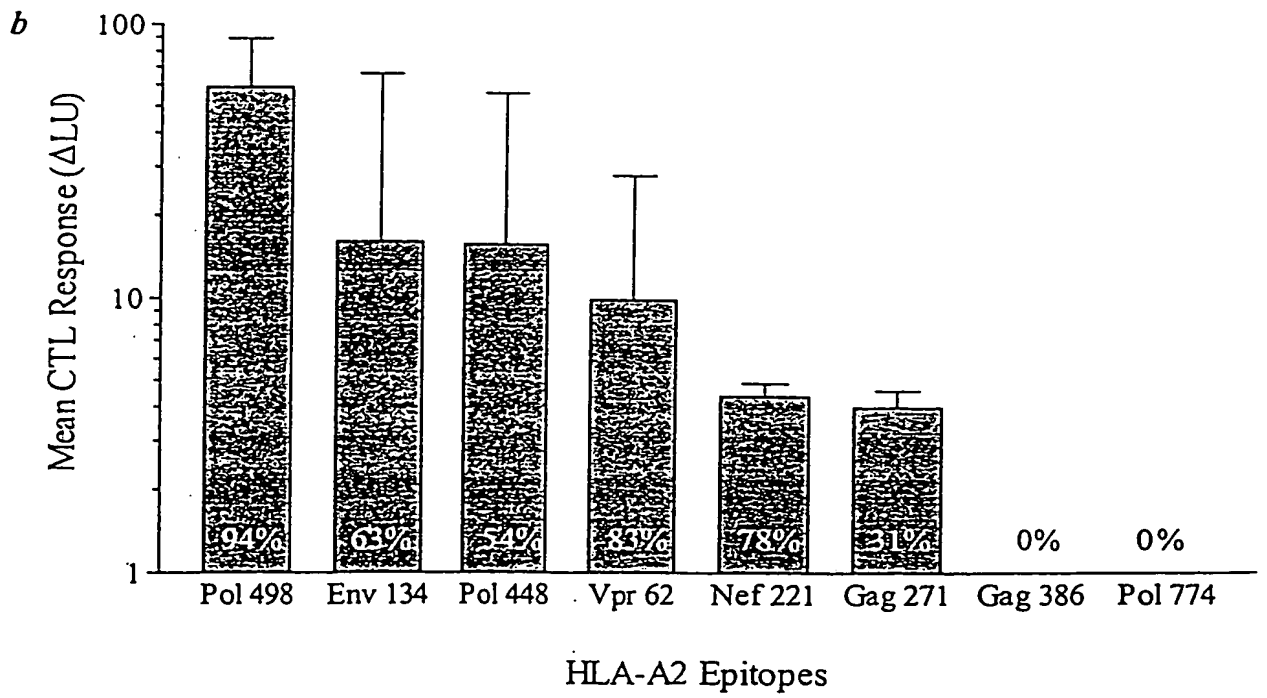
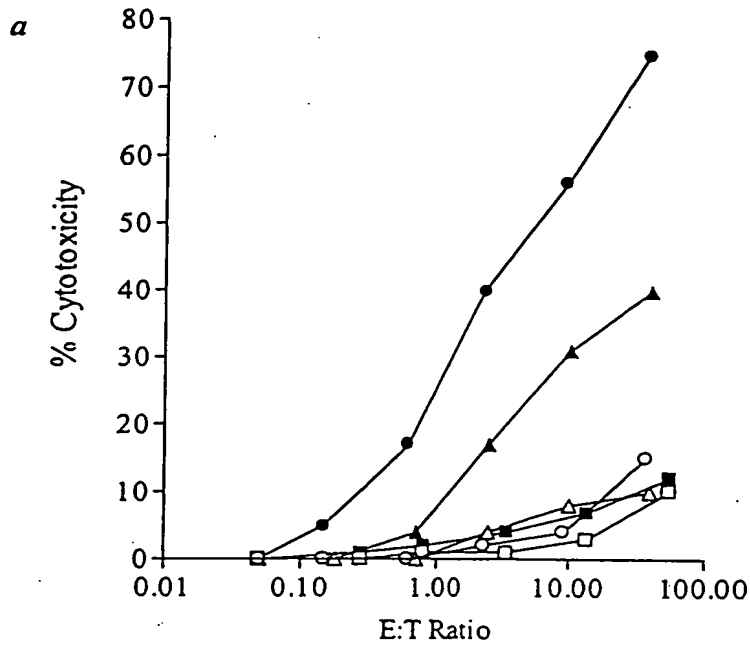


FIGURE 4

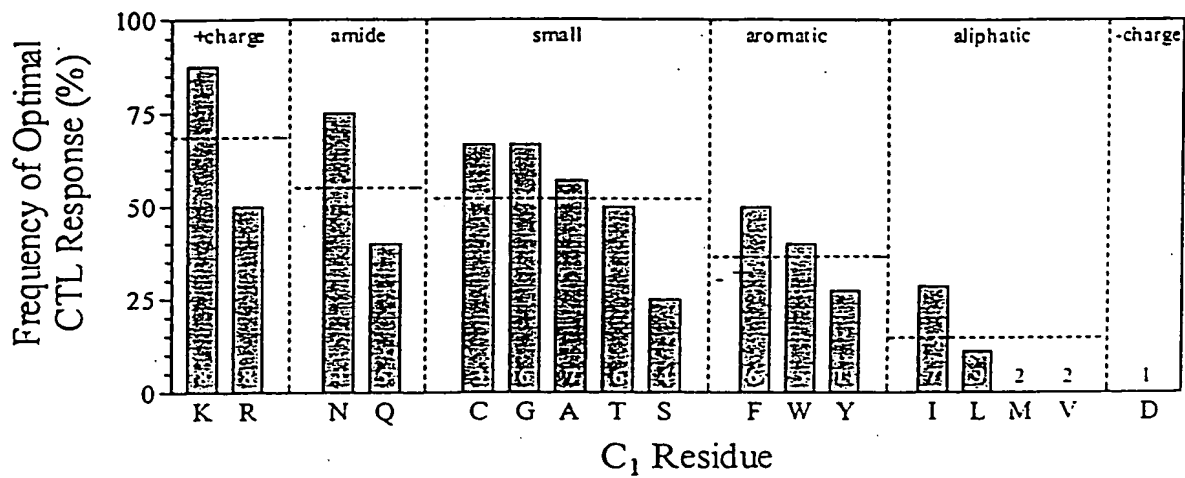
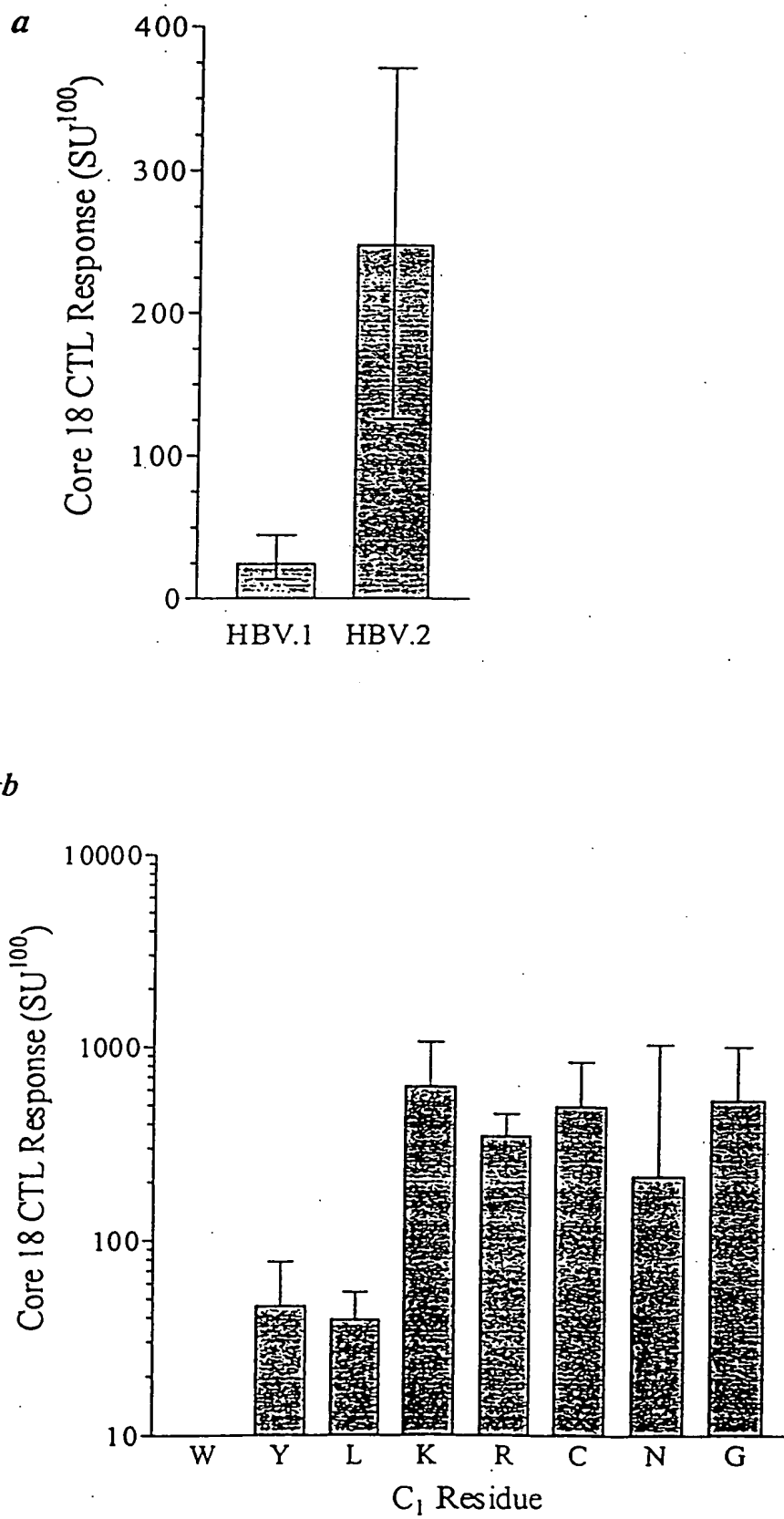


FIGURE 5



FIGURE 6



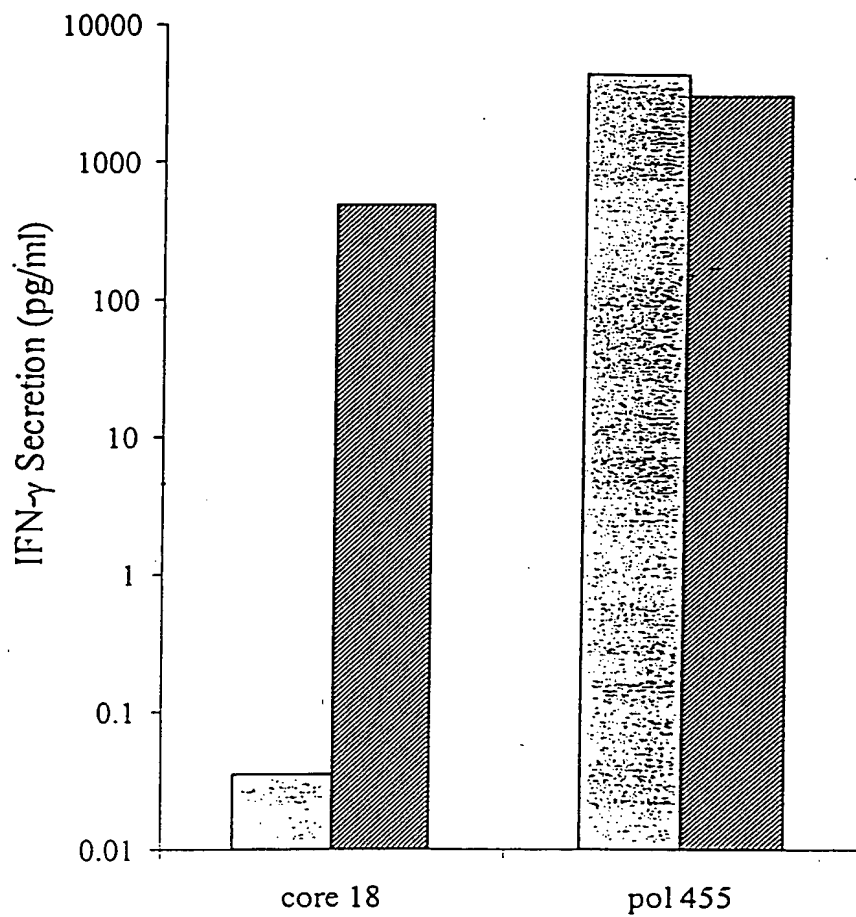


FIGURE 7

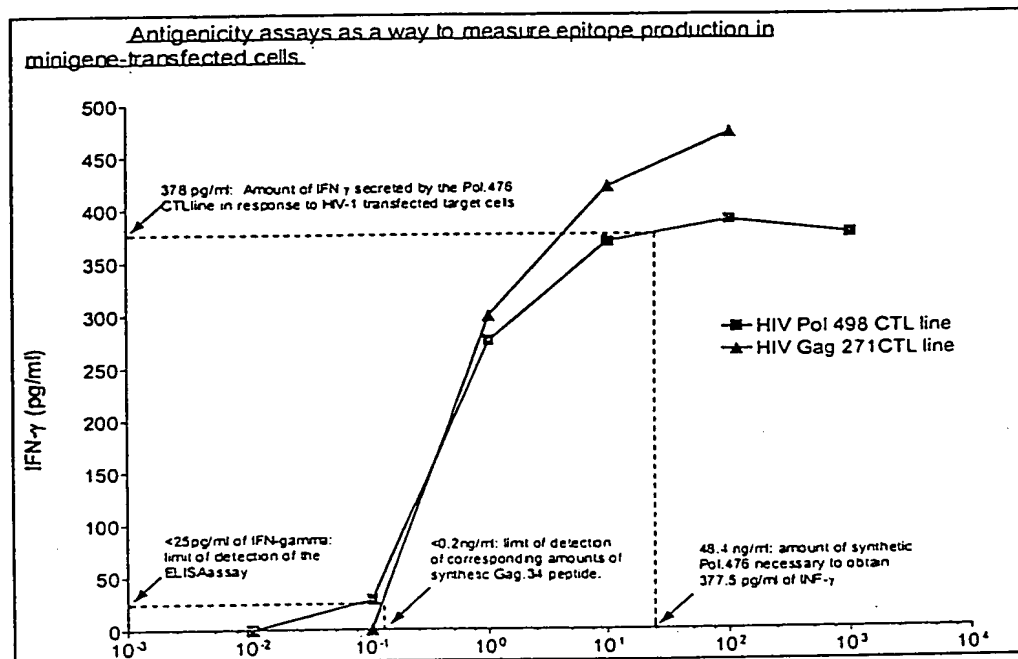
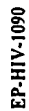


FIGURE 8





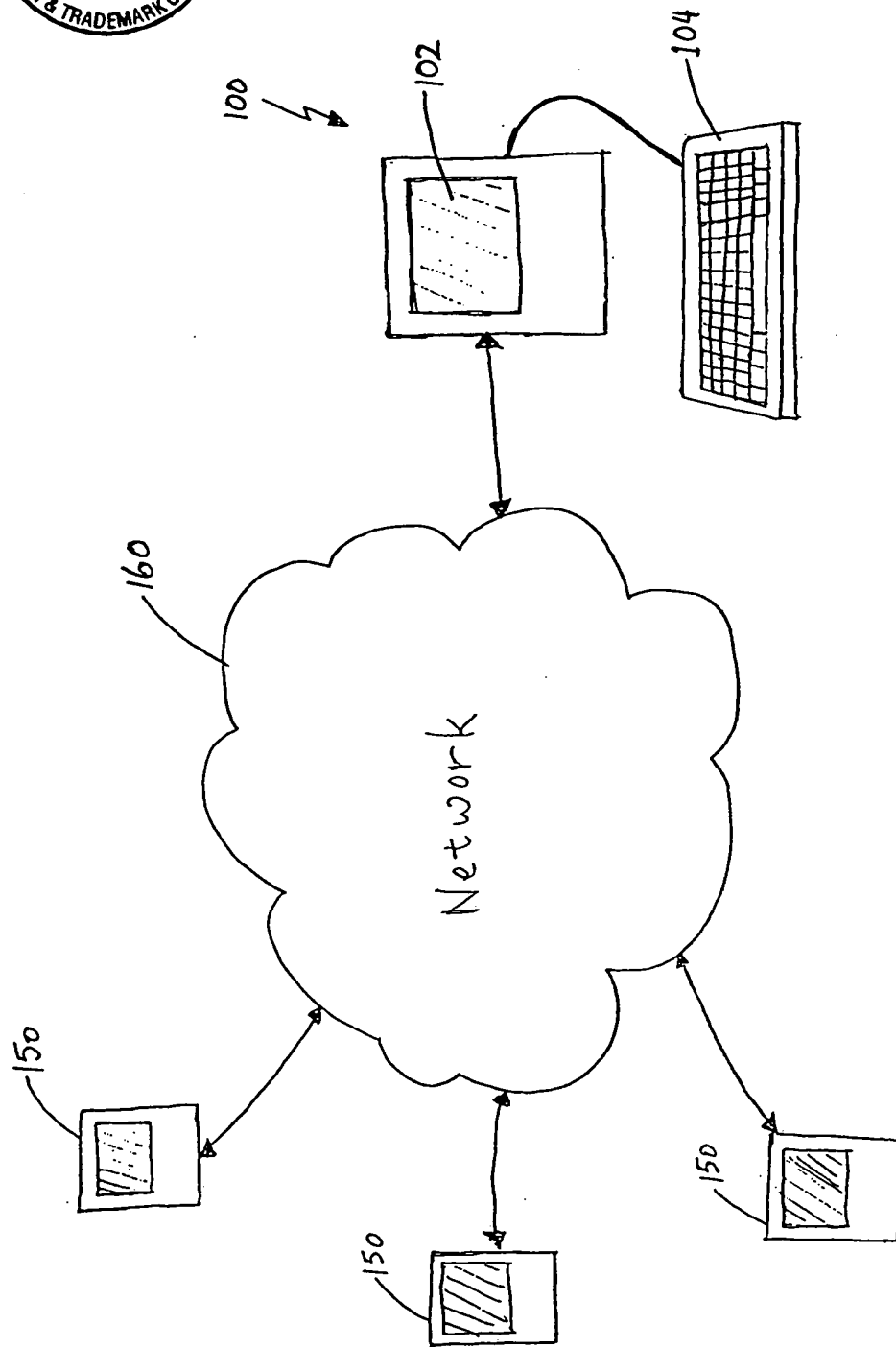


FIGURE 10



200

Sequence	Length	Code
VLA EAMSQV (SEQ ID NO:70)	9	A
ILKEPVHGV (SEQ ID NO:71)	9	B
TLNFPISPI (SEQ ID NO:72)	9	C
SLLNATDIIV (SEQ ID NO:73)	10	D
QMAVFIHNFK (SEQ ID NO:74)	10	E
VTVYYGVVW (SEQ ID NO:75)	11	F
FPVRPQVPL (SEQ ID NO:76)	9	G
YPLASLRSLF (SEQ ID NO:77)	10	H
VTYQYMDDL (SEQ ID NO:78)	10	I
IYQEPFKNL (SEQ ID NO:79)	9	J
IWGCSGKLI (SEQ ID NO:80)	9	K

202

AA	C+1 ranking	N-1 ranking
K	2.20	0.64
C	2.00	1.00
N	2.00	0.00
G	1.80	1.33
T	1.50	0.00
A	1.33	1.21
F	1.33	1.00
S	1.33	0.00
W	1.20	0.00
Q	1.20	0.00
R	1.17	1.57
M	1.00	0.00
Y	1.00	0.75
I	0.86	0.50
L	0.75	2.20
V	0.00	1.19
D	0.00	0.00
H	0.00	0.00
E	0.00	0.00
P	0.00	0.00

204

#### Motif Specification

XXXX(FY)XX(LIMV) (SEQ ID NOS:7-14)  
 XXXX(FY)XXX(LIMV) (SEQ ID NOS:15-22)  
 XXXXNXXX(LIMV) (SEQ ID NOS:27-30)  
 XXXXNXXXX(LIMV) (SEQ ID NOS:341-344)  
 X(LM)XXXXXXV (SEQ ID NOS:31-32)  
 X(LM)XXXXXXV (SEQ ID NOS:33-34)  
 X(LMVT)XXXXXX(KRY) (SEQ ID NOS:345-356)  
 X(LMVT)XXXXXX(KRY) (SEQ ID NOS:357-368)  
 XPXXXXXX(LIMVF) (SEQ ID NOS:59-63)  
 XPXXXXXX(LIMVF) (SEQ ID NOS:64-68)

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FIGURE 11A



MaxInsertions={enter value here} 208  
OutputToScreen=yes/no 210  
OutputToFile=yes/no 212  
MinimumAccepted={enter value here} 214  
MaxDuplicateFunctionValues={enter value here} 216  
MaxSearchTime (min.)={enter value here} 218  
Exhaustive=yes/no 220  
NumStochasticProbes={enter value here} 222  
MaxHitsPerProbe={enter value here} 224  
RandomProbeStart=yes/no 226

**FIGURE 11B**

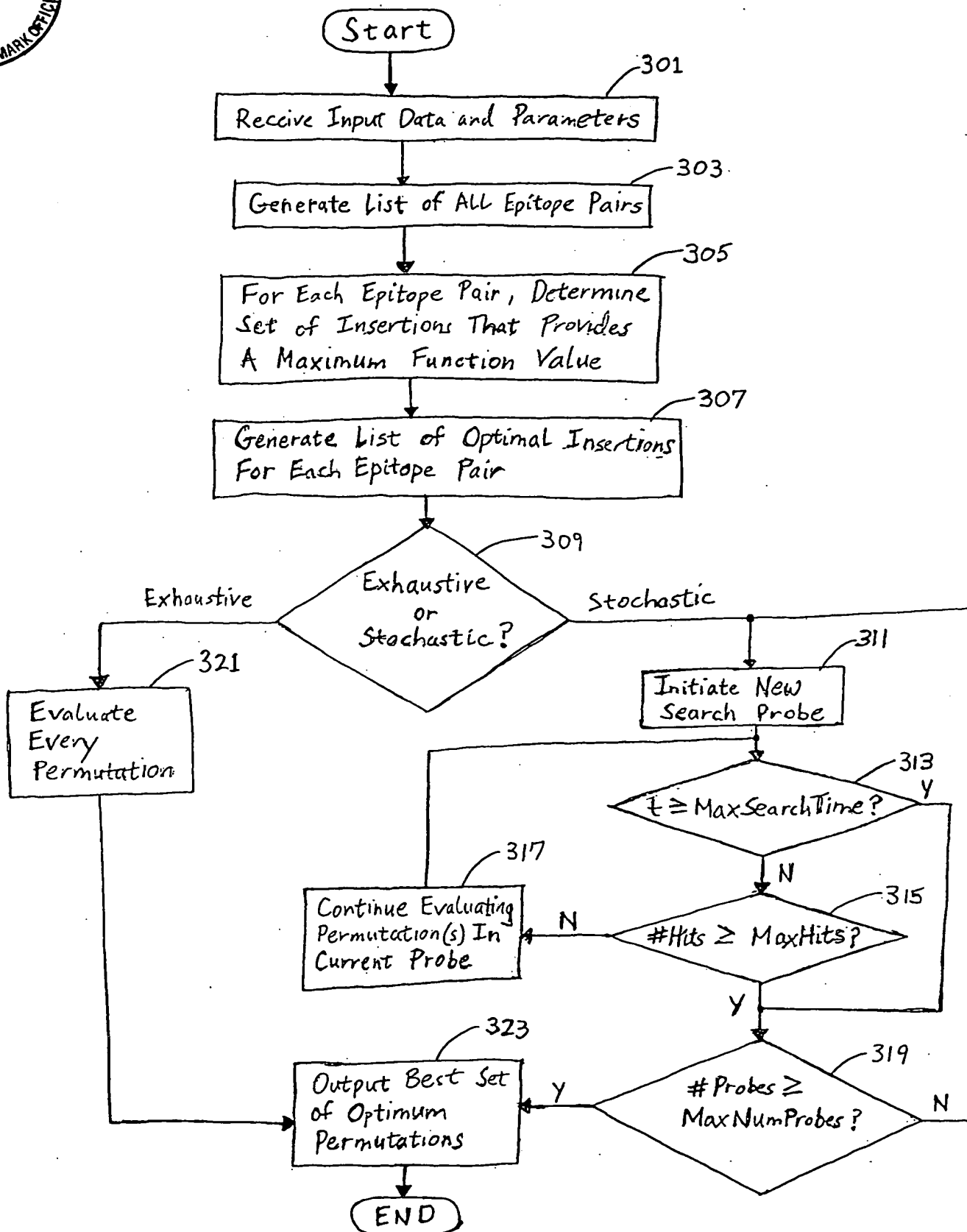


FIGURE 12



Junctional Analyzer run on Saturday, February 26, 2000 09:06:23 pm.

The following non-zero AA weights will be used.

AA	N-1 ranking	C+1 ranking
A	1.21	1.33
C	1.00	2.00
F	1.00	1.33
G	1.33	1.80
I	0.50	0.86
K	0.64	2.20
L	2.20	0.75
M	0.00	1.00
N	0.00	2.00
Q	0.00	1.20
R	1.57	1.17
S	0.00	1.33
T	0.00	1.50
V	1.19	0.00
W	0.00	1.20
Y	0.75	1.00

} 204

The following 10 motif specifications will be used to search for junctionals.

Count	Motif Specification
1	XXXX(FY)XX(LIMV) (SEQ ID NOS:7-14)
2	XXXX(FY)XXX(LIMV) (SEQ ID NOS:15-22)
3	XXXNXXX(LIMV) (SEQ ID NOS:27-30)
4	XXXNXXXX(LIMV) (SEQ ID NOS:341-344)
5	X(LM)XXXXXXV (SEQ ID NOS:31-32)
6	X(LM)XXXXXXV (SEQ ID NOS:33-34)
7	X(LMVT)XXXXXX(KRY) (SEQ ID NOS:345-356)
8	X(LMVT)XXXXXX(KRY) (SEQ ID NOS:357-368)
9	XPXXXXXX(LIMVF) (SEQ ID NOS:59-63)
10	XPXXXXXX(LIMVF) (SEQ ID NOS:64-68)

} 206

Code	Peptide	Length
A	VLA EAMSQV (SEQ ID NO:70)	9
B	ILKEPVHGV (SEQ ID NO:71)	9
C	TLNFPISPI (SEQ ID NO:72)	9
D	SLLNATDIAV (SEQ ID NO:73)	10
E	QMAVFIHNFK (SEQ ID NO:74)	10
F	VTVYYGVPVWK (SEQ ID NO:75)	11
G	FPVRPQVPL (SEQ ID NO:76)	9
H	YPLASLRSLF (SEQ ID NO:77)	10
I	VIIQYMDDL Y (SEQ ID NO:78)	10
J	IYQEPFKNL (SEQ ID NO:79)	9
K	IWGCSGKLI (SEQ ID NO:80)	9

} 202

MaxInsertions = 4 (208)

FIGURE 13A



OutputToScreen = No

OutputToFile = Yes

MinimumValueAccepted = 0

MaxDuplicateFunctionValues = 50

SearchTime = 5

NumStochasticProbes = 10

MaxHitsPerProbe = 25

RandomProbeStart = Yes

Col. 1 Code 1	Col. 2 I1	Col. 3 I2	Col. 4 I3	Col. 5 I4	Col. 6 Code 2	Col. 7 C	Col. 8 N	Col. 9 C+N	Col. 10 J	Col. 11 MaxFunc.
A	C	A		L	B	2.00	2.20	4.40	0	8.80
A	C			L	C	2.00	2.20	4.40	0	8.80
A	C			L	D	2.00	2.20	4.40	0	8.80
A	C			L	E	2.00	2.20	4.40	0	8.80
A	C			R	F	2.00	1.57	3.14	2	1.57
A	C			R	G	2.00	1.57	3.14	1	3.14
A	C			R	H	2.00	1.57	3.14	0	6.28
A	G				I	1.80	1.33	2.39	1	2.39
A	C	A	A	G	J	2.00	1.33	2.66	0	5.32
A	C			R	K	2.00	1.57	3.14	0	6.28
B	C	A	A	G	A	2.00	1.33	2.66	0	5.32
B	C	A		R	C	2.00	1.57	3.14	0	6.28
B	C	A		R	D	2.00	1.57	3.14	0	6.28
B	C	A		R	E	2.00	1.57	3.14	0	6.28
B	C		A	R	F	2.00	1.33	2.66	1	2.66
B	C			R	G	2.00	1.57	3.14	1	3.14
B	C			R	H	2.00	1.57	3.14	0	6.28
B	C	A	A	G	I	2.00	1.33	2.66	1	2.66
B	C	A	A	G	J	2.00	1.33	2.66	0	5.32
B	C	A	A	G	K	2.00	1.33	2.66	0	5.32
C	C	A		R	A	2.00	1.57	3.14	1	3.14
C	C			R	B	2.00	1.57	3.14	1	3.14
C	C	A		L	D	2.00	2.20	4.40	1	4.40
C	C			R	E	2.00	1.57	3.14	1	3.14
C	C			R	F	2.00	1.57	3.14	1	3.14
C	C			R	G	2.00	1.57	3.14	1	3.14
C	C	A		R	H	2.00	1.57	3.14	0	6.28
C	C	A		R	I	2.00	1.57	3.14	1	3.14
C	C	A	A	R	J	2.00	1.57	3.14	0	6.28
C	C	A	A	R	K	2.00	1.57	3.14	0	6.28

FIGURE 13B

MAY 24 2004

PATENT &amp; TRADEMARK OFFICE

Code 1	I1	I2	I3	I4	Code 2	C	N	C+N	J	MaxFunc
D	C			L	A	2.00	2.20	4.40	0	8.80
D	C			L	B	2.00	2.20	4.40	0	8.80
D	C			L	C	2.00	2.20	4.40	0	8.80
D	C			L	E	2.00	2.20	4.40	0	8.80
D	G				F	1.80	1.33	2.39	0	4.79
D	C			R	G	2.00	1.57	3.14	0	6.28
D	C	A	A	G	H	2.00	1.33	2.66	0	5.32
D	C			L	I	2.00	2.20	4.40	1	4.40
D	C	A		R	J	2.00	1.33	2.66	0	5.32
D	C			L	K	2.00	1.57	3.14	0	6.28
E	C	A	A	L	A	2.00	2.20	4.40	0	8.80
E	C	A	A	L	B	2.00	2.20	4.40	0	8.80
E	C	A	A	L	C	2.00	2.20	4.40	0	8.80
E	C	A	A	L	D	2.00	2.20	4.40	0	8.80
E	C	A		R	F	2.00	1.57	3.14	0	6.28
E	C	A		R	G	2.00	1.57	3.14	0	6.28
E	C	A		R	H	2.00	1.57	3.14	0	6.28
E	C	A	A	L	I	2.00	2.20	4.40	0	8.80
E	C	A		R	J	2.00	1.57	3.14	0	6.28
E	C	A		R	K	2.00	1.57	3.14	0	6.28
F	K	A		L	A	2.20	2.20	4.84	1	4.84
F	K	A	A	G	B	2.20	1.33	2.93	1	2.93
F	K	A	A	G	C	2.20	1.33	2.93	0	5.85
F	K	A	A	G	D	2.20	1.33	2.93	0	5.85
F	K	A		G	E	2.20	1.33	2.93	0	5.85
F	K	A		G	G	2.20	1.33	2.93	1	2.93
F	K	A		G	H	2.20	1.33	2.93	1	2.93
F	K		A	R	I	2.20	1.33	2.93	1	2.93
F	K			R	J	2.20	1.57	3.45	1	3.45
G	C	A		R	K	2.20	1.57	3.45	0	6.91
G	C	A		R	A	2.00	1.57	3.14	1	3.14
G	C			R	B	2.00	1.57	3.14	2	1.57
G	C			R	C	2.00	1.57	3.14	1	3.14
G	C	A		L	D	2.00	2.20	4.40	1	4.40
G	C			L	E	2.00	1.57	3.14	2	1.57
G	C			L	F	2.00	2.20	4.40	4	1.10
G	C			G	H	2.00	1.33	2.66	0	5.32
G	C	A	A	R	I	2.00	1.57	3.14	2	1.57
G	C	A	A	R	J	2.00	1.57	3.14	1	3.14
G	C	A	A	R	K	2.00	1.57	3.14	0	6.28
H	C	A	A	G	A	2.00	1.33	2.66	0	5.32
H	C	A		G	B	2.00	1.33	2.66	1	2.66
H	C	A		G	C	2.00	1.33	2.66	0	5.32
H	C	A		G	D	2.00	1.33	2.66	0	5.32
H	C	A	A	G	E	2.00	1.33	2.66	0	5.32
H	C		A	G	F	2.00	1.33	2.66	1	2.66
H	C		A	R	G	2.00	1.57	3.14	1	3.14
H	C	A	A	G	I	2.00	1.33	2.66	1	2.66
H	C	A	A	G	J	2.00	1.33	2.66	1	2.66
H	C		A	G	K	2.00	1.33	2.66	0	5.32

FIGURE 13C



MAY 24 2004

PAT &amp; TRADEMARK

Code 1	I1	I2	I3	I4	Code 2	C	N	C+N	J	MaxFunc
I	K	A	A	G	A	2.20	1.33	2.93	0	5.85
I	K	A	A	G	B	2.20	1.33	2.93	1	2.93
I	K	A		G	C	2.20	1.33	2.93	0	5.85
I	K	A		G	D	2.20	1.33	2.93	0	5.85
I	K	A	A	G	E	2.20	1.33	2.93	0	5.85
I	K	A	A	G	F	2.20	1.33	2.93	1	2.93
I	K	A		R	G	2.20	1.57	3.45	1	3.45
I	K	A	A	G	H	2.20	1.33	2.93	0	5.85
I	K	A	A	G	J	2.20	1.33	2.93	1	2.93
J	K	A	A	R	K	2.20	1.33	2.93	0	5.85
J	K	A	A	R	A	2.20	1.57	3.45	0	6.91
J	K	A	A	R	B	2.20	1.57	3.45	1	3.45
J	K	A		R	C	2.20	1.57	3.45	0	6.91
J	K	A		R	D	2.20	1.57	3.45	0	6.91
J	K	A		R	E	2.20	1.57	3.45	1	3.45
J	K	A	A	R	F	2.20	1.57	3.45	2	1.73
J	K			R	G	2.20	1.57	3.45	1	3.45
J	K		A	R	H	2.20	1.57	3.45	0	6.91
J	K	A	A	R	I	2.20	1.57	3.45	1	3.45
J	K	A	A	R	K	2.20	1.57	3.45	0	6.91
K	K			L	A	2.20	2.20	4.84	0	9.68
K	K			L	B	2.20	2.20	4.84	0	9.68
K	K			L	C	2.20	2.20	4.84	0	9.68
K	K			L	D	2.20	2.20	4.84	0	9.68
K	K	A	A	L	E	2.20	2.20	4.84	0	9.68
K	K	A	A	R	F	2.20	1.57	3.45	1	3.45
K	G				G	1.80	1.33	2.39	0	4.79
K	K			R	H	2.20	1.57	3.45	0	6.91
K	K			L	I	2.20	2.20	4.84	1	4.84
K	K			R	J	2.20	1.57	3.45	0	6.91

Junctional Analyzer took 142.77 seconds.

FIGURE 13D



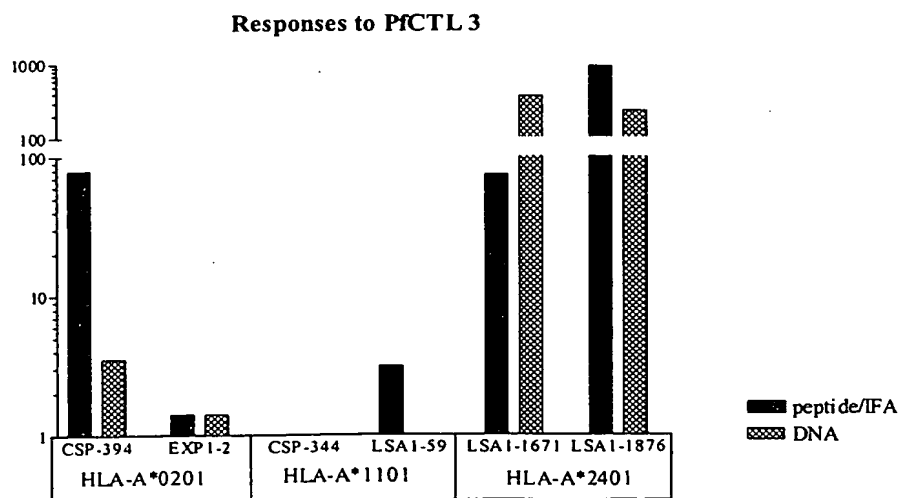
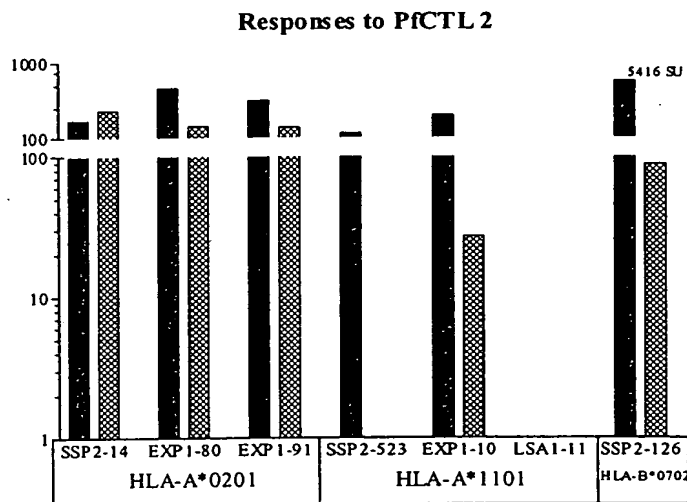
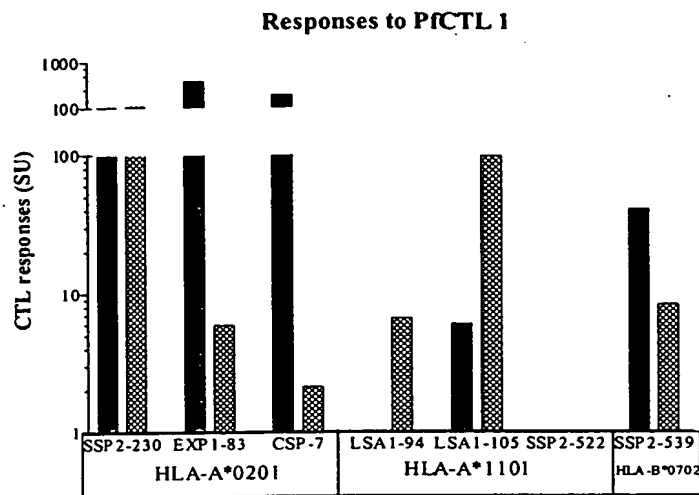


FIGURE 14B

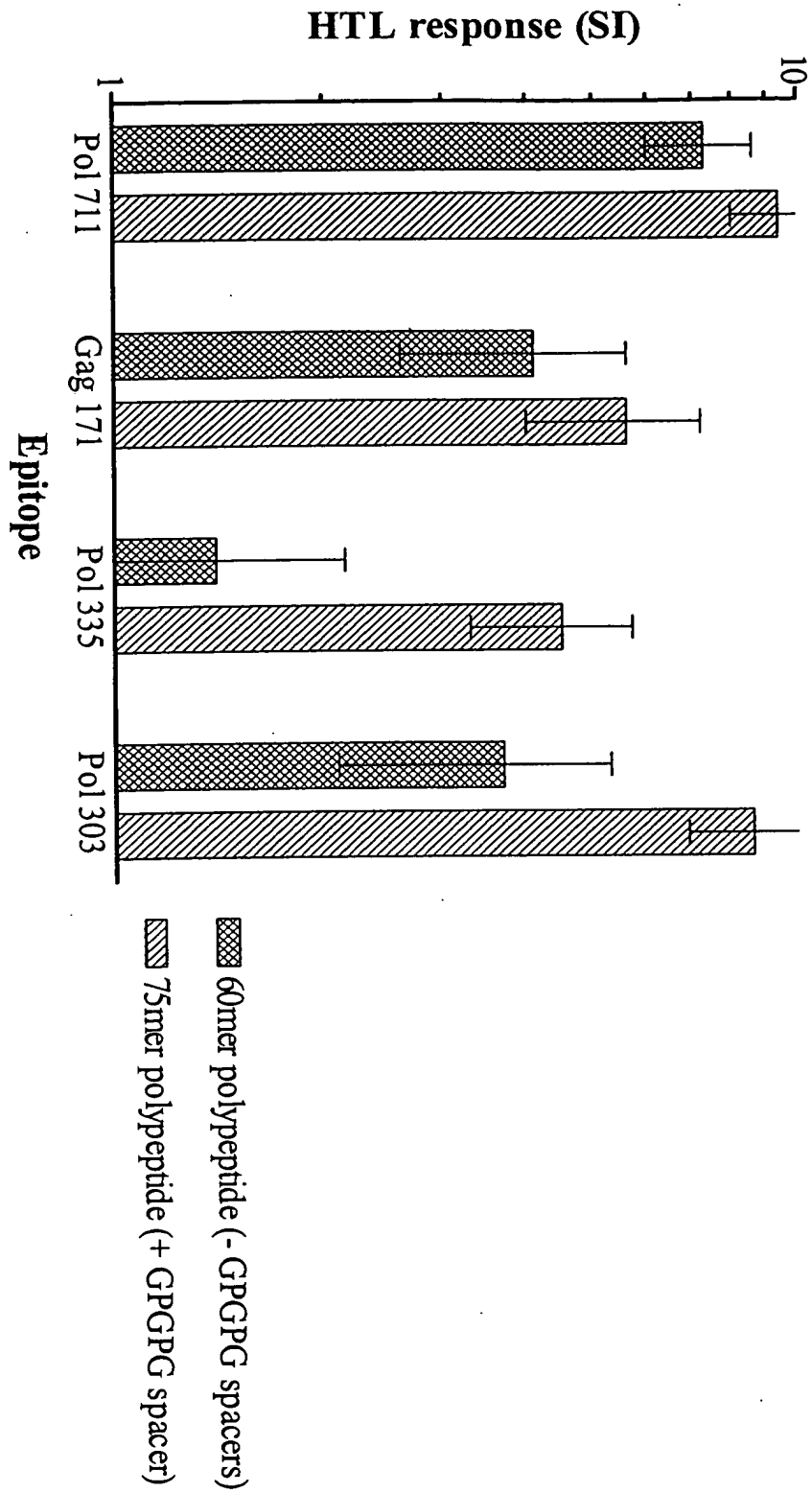


FIGURE 15

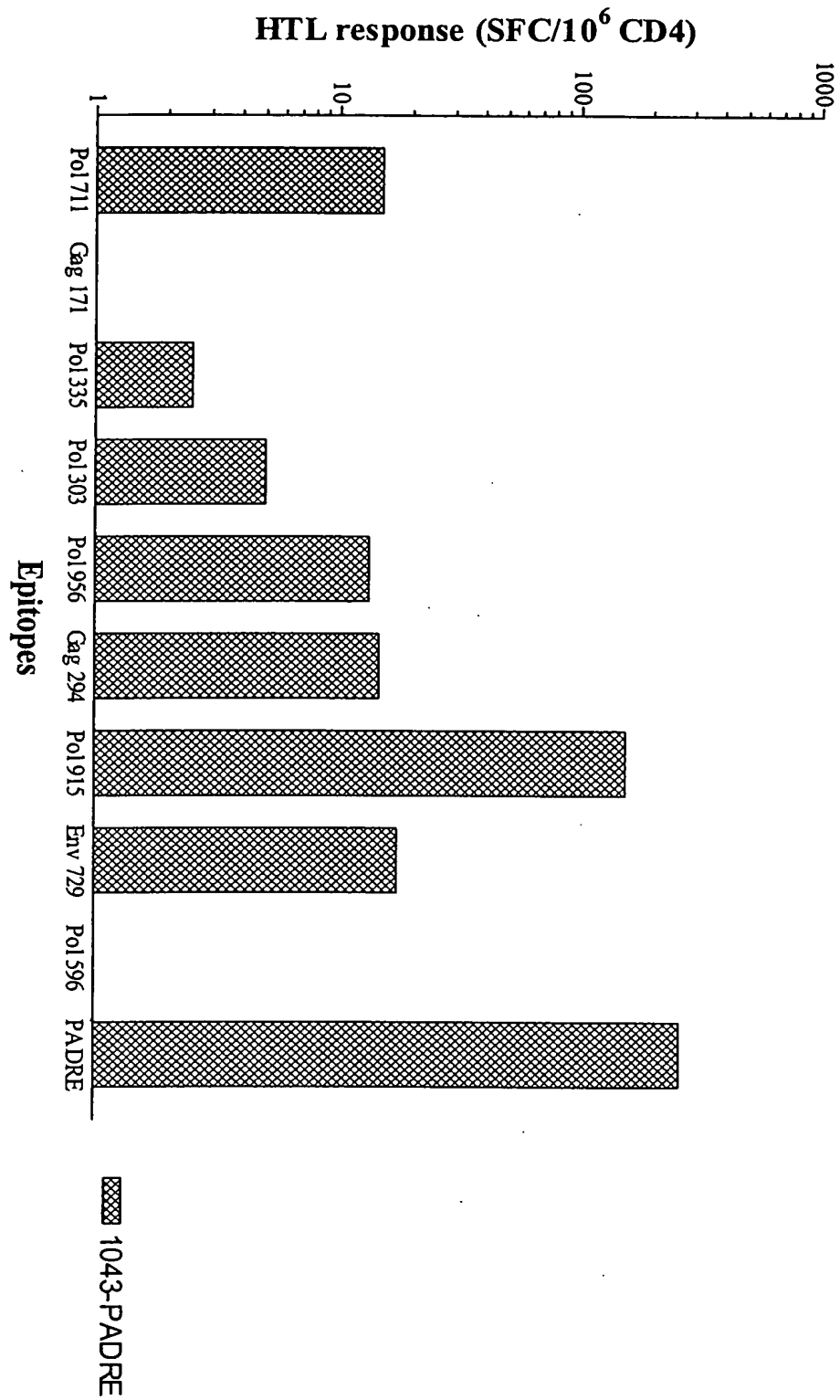


FIGURE 16



HIV 75mer

Pol 711	GAG	Pol 171	GAG	Pol 335	GAG	Pol 303
---------	-----	---------	-----	---------	-----	---------

EP HIV-1043

Pol 711/712	GAG	Pol 956	GAG	Pol 596	GAG	Vpu 31	GAG	Env 729	GAG	Gag 294/298	GAG	Gag 171	GAG	Env 566	GAG	Pol 874	GAG	Pol 915	GAG	Pol 335	GAG	Pol 674	GAG	Pol 758	GAG	Pol 619	GAG	Pol 989	GAG	Pol 303
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EP HIV-1043

Pol 711/712	GAG	Pol 956	GAG	Pol 596	GAG	Vpu 31	GAG	Env 729	GAG	Gag 294/298	GAG	Gag 171	GAG	Env 566	GAG	Pol 874	GAG	Pol 915	GAG	Pol 335	GAG	Pol 674	GAG	Pol 758	GAG	Pol 619	GAG	Pol 989	GAG	Pol 303	GAG	PADRE
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FIGURE 17



EP-HIV-1090 (SEQ ID NO:81)

MGMQVQIQSLFLLLLWVPGSRGKLVGKLNWAGAAILKEPVHGVNAACPKVSFEPIKPIHYCAPA  
KAKFVAAWTLKAAAKAFPVRPQVPLGAAKLTPLCVTLGAAAVLAEAMSQVKVYLAWVPAHKG  
AAAAIFQSSMTKKTTLFCASDAKNIPYNPQSQGVVKHPVHAGPIANVTVYYGVPVWKAAAQMA  
VFIHNFKNAAA YPLASLRSFLNLTFGWCFKLNRLQQLLFINAKIQNFRVYYRKA AVTIKIGGQLKK  
VPLQLPPLKAMTNNPPIPV

ATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCCGGATCCAGA  
GGAAAGCTGGTGGGCAAACTCAACTGGGCCGGAGCTGCAATCCTGAAGGAGCCCCGTCCACGG  
GGTGAATGCCGCTTGCCCTAAAGTCAGCTTCGAACCAATTAAGATCCCCATTCACTACTGTGC  
ACCTGCCAAAGCTAAGTTTGTGGCCGCTTGACCCTCAAGGCCGCTGCAAAAGCCTTCCAGT  
GAGGCCCCAGGTGCCTCTGGGCGCCGCTAAACTCACACCACTGTGCGTCACTCTGGGAGCCGC  
TGCAGTGCTGGCAGAGGCCATGTCCCAAGTGAAGGTGTATCTGGCTTGGGTGCCCCGCCACAA  
GGGGGCCGCTGCAGCCATCTTTCAGTCTAGCATGACCAAGAAAACAACCTCTGTTCTGTGCTC  
CGACGCTAAGAACATCCCTTATAATCCACAGTCTCAGGGCGTGGTCAAGCATCCCGTGCACGC  
CGGACCTATTGCTAACGTGACCGTGTACTATGGGGTCCCAGTGTGGAAGAAAGCCGCTGCACA  
GATGGCCGTGTTTATTACAAATTTCAAAAACGCCGCTGCATACCCCCTCGCCAGCCTGAGATC  
CCTCTTCAACCTGACATTCGGCTGGTGTCTTAAGCTGAACCGGATCCTGCAGCAACTGCTCTTT  
ATCAATGCTAAAATCCAGAACTTCCGCGTCTACTATAGGAAGGCTGCAGTGACTATCAAAATT  
GGCGGACAACTGAAGAAAGTGCTCTCCAGCTGCCCCCTCTCAAGGCAATGACCAACAATCC  
CCCTATCCCAGTCTGA (SEQ ID NO:82)

HIV-CPT (SEQ ID NO:83)

MGMQVQIQSLFLLLLWVPGSRGIPHYCAPAKAAKIQNFRVYYRKA AVTIKIGGQLKKAKFVAAW  
TLKAAAKVPLQLPPLKAIFQSSMTKLTPLCVTLGAQMAVFIHNFKGAKVYLAWVPAHKNAIPYN  
PQSQGVVKAILKEPVHGVGAAALTFGWCFKLNAVLAEMSQVNRILQQLLFINAAACPKVSFEPI  
KVTVYYGVPVWKKAAHPVHAGPIANAAA YPLASLRSFLNAAATTLFCASDAKNKLVGKLNWAN  
AAAFPVRPQVPLNMTNNPPIPV

ATGGGGATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCCGGATCCAGA  
GGAATCCCCATTCACTACTGCGCCCCCTGCTAAGGCAGCCAAAATCCAGAACTTCAGGGTGTAT  
TACAGAAAGGCTGCAGTCACCATTAATAATCGGCGGACAACTGAAGAAAGCCAAGTTTGTGGC  
CGCTTGACACTCAAGGCCGCTGCAAAGGTCCCACTGCAGTCCCCCTCTGAAGGCCATCTT  
CCAGAGCTCCATGACTAAGAAACTGACCCCACTGTGTGTGACACTCGGGGCCAGATGGCTGT  
GTTCATCCATAATTTTAAAGGCGCCAAGGTCTACCTGGCTTGGGTGCCCCGCACACAAGAACGC  
CATTCCTTACAATCCACAGTCTCAAGGAGTGGTCAAAGCTATTCTGAAGGAGCCCGTGCACGG  
GGTGGGCGCCGCTGCACTCACTTTCCGATGGTGTCTTAAACTGAACGCCGTGCTGGCTGAAGC  
CATGAGCCAGGTCAATCGGATCCTGCAGCAACTGCTCTTCAATTAACGCCGCTGCATGTCCTAA  
GGTGTCTTTCGAGCCAATCAAAGTGACCGTGTATTACGGGGTCCCCGTGTGGAAGAAAGCCGC  
TCATCCTGTCCACGCAGGCCCAATCGCCAACGCCGCTGCATATCCCCTCGCCTCTCTGCGCAG  
CCTGTTTAAACGCCGCTGCAACAACCTCTTTTGCGCCTCCGACGCTAAGAATAAACTGGTGGG  
AAAGCTGAAGTGGGCCAACGCAGCTGCATTCCCTGTGAGGCCACAGGTCCCCCTCAATATGAC  
TAACAATCCCCCTATCCCAGTGTGA (SEQ ID NO:84)

FIGURE 18A



HIV-FT (SEQ ID NO:85)

MQVQIQSLFLLLLWVPGSRGKLVGKLNWAMASDFNLPPVAIFQSSMTKVTIKIGGQLKRILQQLLF  
IMAVFIHNFKIPYNPQSQGVVTTLFCASDAKILKEPVHGVQMAVFIHNFKGAAVFIHNFKRCPKVSF  
EPIKIQNFRVYYRLTFGWCFKLQVPLRPMTYKMTNNPPIPVTVYYGVPVWKVLAEAMSQVPIHY  
CAPAKLTPLCVTL

ATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCCGGATCCAGAGGAAAG  
CTGGTGGGGAAGCTGAACTGGGCCATGGCCAGCGATTTC AACCTGCCCCCGTGGCCATCTTC  
CAGAGCAGCATGACCAAGGTGACCATCAAGATCGGGGGGCAGCTGAAGAGGATCCTGCAGCA  
GCTGCTGTTTCATCATGGCCGTGTTTCATCCACA ACTTCAAGATCCCCTACAACCCCAAGAGCCA  
GGGGGTGGTGACCACCCTGTTCTGCGCCAGCGATGCCAAGATCCTGAAGGAGCCCGTGACG  
GGGTGCAGATGGCCGTGTTTCATCCACA ACTTCAAGGGCGCCGCGTGTTCATCCACA ACTTCA  
AGAGGTGCCCCAAGGTGAGCTTCGAGCCCATCAAGATCCAGAACTTCAGGGTGTACTACAGG  
CTGACCTTCGGGTGGTGCTTCAAGCTGCAGGTGCCCCCTGAGGCCCATGACCTACAAGATGACC  
AACAACCCCCCATCCCCGTGACCGTGTACTACGGGGTGCCCGTGTGGAAGGTGCTGGCCGAG  
GCCATGAGCCAGGTGATCCCCATCCACTACTGCGCCCCCGCCAAGCTGACCCCCCTGTGCGTG  
ACCCTG (SEQ ID NO:86)

**FIGURE 18B**





HIV-TC (SEQ ID NO:87)

MGMQVQIQSLFLLLLWVPGSRGYWQATWIPEWKAIFQSSMTKKVYLAWVPAHKNAACPKVSFE  
PIKHPVHAGPIANLTFGWCFKLNKMIGGIGGFIKFRDYVDRFYKAAARILQQLLFINTTLFCASDAK  
NQMVHQAI SPRGAKLVGKLNWAGAAAIYETYGDTWKAAQVPLRPMTYKGAAAVTVLDVGDAY  
NAAARYLKDQQLNLNFPISPINMTNPPIPVNAPYNTPVFAIKAAAVPLQLPPLKAAIPYNPQSQ  
GVVKALLQLTVWGIGAILKEPVHGVNAAAFPIPIETVKVWKEATTTLFKAAAVTIKIGGQLKKI  
YQEPFKNLAAAFLAEAMSQVNLVGPTPVNIGAAAEVNIVTDSQYKAAAPIHYCAPAKAVIYQY  
MDDLKAAAQMAVFIHNFKNAAATYQIYQEPFKPYNEWTLKAKIQNFRVYYRKAFVVRPQVPL  
GAAAIWGC SGKLIKVMIVWQVDRNAAKAACWWAGIKAKFVAAWTLKAAAKLTPLCVTLNAAM  
ASDFNLPPVKSLLNATDIAVNVTVYYGVPVWKKAAAAIIRILQQLKRAMASDFNLNAAAYPLASL  
RSLF

ATGGGGATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGATCTAGA  
GGATACTGGCAAGCTACTTGGATTCCAGAATGGAAAGCTATCTTTCAATCCTCAATGACGAAG  
AAGGTATACCTGGCATGGGTCCCAGCACACAAGAACGCCGCTTGCCCAAAGGTGTCCTTTGAA  
CCCATTAACACCCAGTGCACGCAGGGCCAATAGCGAATTTGACATTGGGTGGTGCTTCAAA  
CTAAACAAAAATGATCGGCGGCATTGGAGGCTTTATCAAGTTTAGAGATTACGTGGACCGATT  
TATAAAGCCGCTGCCGTATACTCCAGCAGCTACTATTCAACACCACTCTCTTCTGCGCTT  
CAGACGCTAAGAACCAATGGTACACCAAGCCCTAGAGGAGCCAAGCTCGTAGGG  
AAATTAATTTGGGCGGGTGCAGCAGCAATCTACGAGACTTACGGCGATACCTGGAAAGCAGC  
CCAGGTTCCGTTACGCCAATGACCTATAAAGGCGCAGCAGCAGTAACAGTTCTAGATGTAGG  
AGACGCTTACAACGCTGCCGCAAGATACCTAAAAGATCAGCAGTTACTCAACACACTAAATTT  
CCCAATTAGCCCGATAAACATGACAAATAACCCACCAATTCCCGTCAATGCTCCCTACAACAC  
TCCAGTATTCGCAATCAAAGCCGCTGCTGTCCCCCTGCAGCTCCCTCCTCTGAAAGCTGCGAT  
ACCTTACAACCCACAGAGCCAAGGTGTTGTCAAAGCACTGCTTCAGCTAACAGTTTGGGGAAT  
TGGTGCTGCAATTCTAAAAGAGCCAGTTCATGGGGTTAACGCCGCCGCTTCCCAATCAGTCC  
TATTGAGACTGTGAAAGTATGGAAAGAAGCCACAACCACACTTTTTAAGGCAGCCGCAGTTA  
CAATTAATAATAGGGGGCCAACTTAAGAAAAATATACCAGGAACCTTTCAAGAATCTCAAAGCC  
GCTGCAGTGCTCGCCGAGGCTATGTACAGGTGAATTTGGTGGACCAACACCCGTAAACATC  
GGAGCCGCAGCCGAAGTGAACATAGTACCCGACTCACAGTACAAAGCCGCTGCAATACCCAT  
ACATTATTGTGCTCCCGCAAAGGCCGTGATCTATCAATATATGGACGACCTGTATAAGGCCGC  
CGCGCAGATGGCAGTCTTTATCCACAACCTTTAAAAACGCAGCTACTTATCAGATCTACCAGGA  
ACCATTCAAACCGTACAATGAGTGGACCTTGGAATAAAGGCCAAAATTCAGAACTTCAGGG  
TATATTATAGAAAAGCATTTCCAGTGAGGCCCCAGGTGCCTCTGGGTGCCGCAGCAATATGGG  
GATGTTCTGGAAAAGTATCAAGGTGATGATTGTATGGCAAGTGGACAGAAATGCAGCTAAG  
GCAGCCTGTTGGTGGGCAGGTATAAAGCAAAGTTCGTGGCAGCATGGACGCTTAAAGCAGC  
CGCAAAACTCACTCCTCTCTGCGTGACACTTAATGCAGCCATGGCCTCTGATTTCACCTTCCC  
CCTGTAAAATCCCTGCTTAATGCGACAGATATCGCAGTCAACGTAACAGTATATTATGGCGTG  
CCAGTCTGGAAAAAAGCCGCCGCGGCCATAATTCGGATACTGCAGCAGCTGAAAAGAGCTAT  
GGCGAGTGACTTCAACCTGAATGCGGCCGCTACCCCTTGGCATCGTTAAGGTCATATTTTG  
A (SEQ ID NO:88)

FIGURE 18C



HCV.1 (SEQ ID NO:89)

MGMQVQIQSLFLLLLWVPGSRGLLFNILGGWVDLMGYIPLVYL VAYQATVILAGYGAGVRLIVFP  
DLGVHMWNFISGIYLLPRRGPRLYL VTRHADVVLVGGVLAALLFLLLADAFLLLADARVWMNRL  
IAFACTCGSSDLYLSAFSLHSYG VAGALVAFKLP GCSFSIFKTSERSQPRLIFCHSKKKFWAKH MW  
NFIPFYGKAIRMYVGGVEHRQLFTFSRRRLGVRATRKVG IYLLPNRAKFVAAWTLKAAA\*

GAATTCGCCGCCACCATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGATCCAGAGGACTGC  
TGTTCAACATCCTGGGGGGTGGGTGGATCTGATGGGTACATCCCCCTGGTGTACCTGGTGGCCTACCAGGCCACCGT  
GATCCTGGCCGGGTACGGGGCCGGGTGAGGCTGATCGTGTTCCTGCTGCTGGGTGCACATGTGGAACCTTCATCAGC  
GGGATCTACCTGCTGCCAGGAGAGGACCTAGACTGTACCTGGTACTAGACACGCTGATGTGGTGTCTGGTGGGAGGAG  
TGCTGGCTGCTCTGCTGTTTCTGCTGCTGGCTGATGCTTTCCTGCTGCTGGCTGATGCTAGAGTGTGGATGAACAGACT  
GATCGCTTTTCGCTTGATACATGTGGAAGCTCCGATCTGTATCTGAGCGCTTTCAGCCTGCACAGCTACGGAGTGGCTGGA  
GCTCTGGTGGCTTTTAAGCTGCCTGGATGTAGCTTTAGCATCTTTAAGACCAGCGAAAGAAGCCAGCCTAGACTGATCT  
TTTGTACAGCAAGAAGAAGTTTGGGCTAAGCACATGTGGAATTTTATCCCTTTCTATGGAAGGCTATCAGAATGTA  
TGTGGGAGGAGTGGAAACACAGACAGCTGTTTACATTTAGCCCTAGAAGGAGACTGGGAGTGAGAGCTACAAGAAAGGTG  
GGAATCTATCTGCTGCCTAATAGATGAAAGCTTGGG\* (SEQ ID NO:90)

HCV.2 (SEQ ID NO:91)

MGMQVQIQSLFLLLLWVPGSRGDLMGYIPLVAKFVAAWTLKAAALLFLLLADALIFCHSKKKQLF  
TFSPRRYL VTRHADVYLLPRRGPRLCTCGSSDLYHMWNFISGIFWAKH MWNF AKFVAAWTLKAA  
AILAGYGAGVYL VAYQATVGVAGALVAFKIPFYGKAIRMYVGGVEHRVLVGGVLAALFLLLADA  
RVLP GCSFSIFAKFVAAWTLKAAAKTSERSQPRRLGVRATRKRLIVFPDLGVWMNRLIAFALSAFS  
LHSYLLFNILGGWVVG IYLLPNR\*

GAATTCGCCGCCACCATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGG  
GTGCCCGGATCCAGAGGAGATCTGATGGGATATATCCCTCTGGTGGCTAAGTTTGTGGCTGCT  
TGGACACTGAAGGCTGCTGCTGCTGTTTCTGCTGCTGGCTGATGCTCTGATCTTCTGT CACA  
GCAAGAAGAAGCAGCTGTTTACATTTAGCCCAAGAAGATATCTGGTGACAAGACACGCTGAT  
GTGTATCTGCTGCCTAGACGCGGACCTAGACTGTGTACATGTGGAAGCTCCGATCTGTATCAC  
ATGTGGAACCTTTATCAGCGGAATCTTTTGGGCTAAGCACATGTGGAATTTTCATCCTGGCTGGA  
TATGGAGCTGGAGTGTATCTGGTGGCTTATCAGGCTACAGTGGGAGTGGCTGGAGCTCTGGTG  
GCTTTCAAGATCCCATTCTATGGAAGGCTATCAGAATGTATGTGGGAGGAGTGGAAACACAG  
AGTGCTGGTGGGAGGAGTGCTGGCTGCTTTCCTGCTGCTGGCTGATGCTAGAGTGCTGCCAGG  
ATGTAGCTTTAGCATCTTCAAGACTTCCGAACGCTCCAGCCTAGAAGACTGGGAGTGAGAGC  
TACAAGGAAGAGACTGATCGTGTTCAGATCTGGGAGTGTGGATGAATAGACTGATCGCTTT  
CGCTCTGAGCGCTTTCAGCCTGCACAGCTATCTGCTGTTCAACATCCTGGGAGGATGGGTGGT  
GGGAATCTATCTGCTGCCAAACAGATGAAAGCTT (SEQ ID NO:92)

HCV.3s1 (SEQ ID NO:93)

MGMQVQIQSLFLLLLWVPGSRGYLVAYQATVAKFVAAWTLKAAALLFLLLADALIFCHSKKKYL  
VTRHADVLGFGAYMSKCTCGSSDLYHMWNFISGIFWAKH MWNF\*

GAATTCGCCGCCACCATGGGAATGCAGGTGCAGATCCAAAGCCTGTTTCTGCTCCTCCTGTGG  
GTGCCCGGATCCAGAGGATACCTCGTCGCCTACCAGGCCACTGTGGCTAAATTCGTGGCAGCC  
TGGACACTGAAAGCTGCAGCTCTGCTCTTCTGCTCCTGGCCGATGCACTCATCTTCTGCCATT  
CCAAGAAAAAGTATCTGGTCAACAGACATGCTGACGTGCTGGGGTTTGGCGCCTACATGAGC  
AAGTGACCTGTGGCAGCTCCGACCTGTATCACATGTGGAACCTTTATTTCTGGAATCTTTTGGG  
CCAAGCACATGTGGAATTTCTGAAAGCTT (SEQ ID NO:94)

FIGURE 18D



HCV.3s2 (SEQ ID NO:95)

MGMQVQIQSLFLLLLWVPGSRGVLVGGVLAAAFVAAWTLKAAAFLLLADARVLSAFSLHSYIL  
AGYGAGVWMNRLIAFAIPFYGKAIVAGALVAFKVGIYLLPNR\*

GAATTCGCCGCCACCATGGGAATGCAGGTGCAGATCCAAAGCCTGTTTCTGCTCCTCCTGTGG  
GTGCCCCGATCCAGAGGAGTCCTGGTGGGCGGCGTCCTGGCCGCTGCTAAGTTTGTGCGCTGCT  
TGGACACTGAAGGCAGCCGCTTCTGCTCCTGGCAGACGCCAGGGTGCTGTCTGCCTTCAGC  
CTCCACTCCTACATCCTCGCAGGGTATGGCGCAGGCGTGTGGATGAATCGGCTGATCGCCTTT  
GCCATTCCATTCTATGGGAAAGCCATTGTGGCTGGCCCTGGTGGCATTCAAGGTCGGGATC  
TACCTCCTGCCTAACCCTGAAAGCTT (SEQ ID NO:96)

HCV.3s2(-3) (SEQ ID NO:97)

MGMQVQIQSLFLLLLWVPGSRGVLVGGVLAAAFVAAWTLKAAAFLLLADARVLSAFSLHSYIL  
AGYGAGVWMNRLIAFA\*

GAATTCGCCGCCACCATGGGAATGCAGGTGCAGATCCAAAGCCTGTTTCTGCTCCTCCTGTGG  
GTGCCCCGATCCAGAGGAGTCCTGGTGGGCGGCGTCCTGGCCGCTGCTAAGTTTGTGCGCTGCT  
TGGACACTGAAGGCAGCCGCTTCTGCTCCTGGCAGACGCCAGGGTGCTGTCTGCCTTCAGC  
CTCCACTCCTACATCCTCGCAGGGTATGGCGCAGGCGTGTGGATGAATCGGCTGATCGCCTTT  
GCCTGAGGATCC (SEQ ID NO:98)

HCV.3s3 (SEQ ID NO:99)

MGMQVQIQSLFLLLLWVPGSRGDLMGYIPLVAKFVAAWTLKAAARLGVRATRKLLFNILGGWV  
RMVYGGVEHRRLLIVFPDLGVGVAGALVAFKLPGCSFSIFKTSERSQPRQLFTFSPPRYLLPRRGPRL

GAATTCGCCGCCACCATGGGAATGCAGGTGCAGATCCAAAGCCTGTTTCTGCTCCTCCTGTGG  
GTGCCCCGATCCAGAGGAGACCTGATGGGCTACATCCCTCTCGTGGCCAAGTTTGTGGCAGCT  
TGGACCCTGAAGGCCGCTGCCAGACTGGGAGTGCGCGCTACACGGAAACTCCTGTTTAACATC  
CTGGGAGGGTGGGTGCGGATGTACGTCGGAGGCGTCGAGCACAGAAGGCTCATTGTCTTTCC  
AGATCTCGGCGTGGGCGTCGCAGGCGCACTCGTGGCCTTCAAACCTGCCAGGGTGCAGCTTCAG  
CATTTTCAAGACCTCCGAACGCTCCCAACCCAGACAGCTGTTCACTTTCTCTCCTCGGAGGTAT  
CTGCTGCCAGACGCGGACCCAGGCTGTGAAAGCTT (SEQ ID NO:100)

HCV.PC3 (SEQ ID NO:101)

MGMQVQIQSLFLLLLWVPGSRGLLFNILGGWVKAKFVAAWTLKAAALADGGCSGGAYRLIVFPD  
LGVKFWAKHMWNFIGVAGALVAFKKQLFTFSPPR\*

GAATTCGCCGCCACCATGGGAATGCAGGTGCAGATCCAAAGCCTGTTTCTGCTCCTCCTGTGG  
GTGCCCCGATCCAGAGGACTGCTCTTCAACATCCTGGGCGGATGGGTGAAGGCCAAGTTCGTG  
GCTGCCTGGACCCTGAAGGCTGCCGCTCTGGCCGACGGGGATGCAGCGGCGGAGCTTACAG  
GCTCATTGTCTTTCCCGATCTCGGAGTCAAATTTTGGGCAAAGCACATGTGGAATTTTCATCGG  
GGTGGCCGAGCCCTGGTCGCTTTTAAAAGCAGCTCTTACCTTCTCCCAAGACGGTGAGG  
TACC (SEQ ID NO:102)

FIGURE 18E



HCV\_PC4 (SEQ ID NO:103)

MGMQVQIQSLFLLLLWVPGSRGRLGVRATRKKAKFVAAWTLKAAAKTSERSQPRNLPGCSFSIFN  
DLMGYIPLVKYLLPRRGPRLNTLCGFADLMGYRMYVGGVEHR\*

GAATTCGCCGCCACCATGGAATGCAGGTGCAGATCCAAAGCCTGTTTCTGCTCCTCCTGTGG  
GTGCCCCGGATCCAGAGGAAGGCTGGGCGTGAGAGCCACCCGGAAGAAGGCCAAGTTCGTGGC  
TGCTGGACCTGAAGGCTGCCGCTAAAACAAGCGAGCGCTCCCAGCCCAGGAACCTGCCTG  
GATGCTCTTTACGATCTTTAATGACCTCATGGGGTACATTCCACTGGTGAAGTATCTGCTCCC  
CAGACGGGGCCCTCGCCTGAAOACTCTCTGTGGATTGCTGATCTGATGGGGTACAGGATGTA  
TGTCGGCGGAGTCGAACACAGATGAGGTACC (SEQ ID NO:104)

HCV\_2431(1P) (SEQ ID NO:105)

MGMQVQIQSLFLLLLWVPGSRGVLVGGVLAAFLLLADARVLSAFSLHSYILAGYGAGVWMNRL  
IAFAGAAARLGVRATRKKAAAKTSERSQPRNLPGCSFSIFNDLMGYIPLVKYLLPRRGPRLNTLCG  
FADLMGYRMYVGGVEHRKLLFNILGGWVKAAALADGGCSGGA YRLIVFPDLGVKFWAKHMWN  
FIGVAGALVAFKKQLFTFSPPRNGYLVA YQATVAAALLFLLADALIFCHSKKKYL VTRHADVLG  
FGAYMSKCTCGSSDL YHMWNFISGIFWAKHMWNFKAAA AKFVAAWTLKAAA

GAATTCGCCGCCACCATGGAATGCAGGTGCAGATCCAAAGCCTGTTTCTGCTCCTCCTGTGG  
GTGCCCCGGCTCCAGAGGAGTCCTGGTGGGCGGCGTCCTGGCAGCCGCTTTCCTGCTCCTGGCA  
GACGCCAGGGTGCTGTCTGCCTTCAGCCTCCACTCCTACATCCTCGCAGGGTATGGCGCAGGC  
GTGTGGATGAATCGGCTGATCGCCTTTGCCGGCGCTGCCGCAAGGCTGGGCGTGAGAGCCACC  
CGAAGAAGGCTGCCGCTAAAACAAGCGAGCGCTCCCAGCCCAGGAACCTGCCTGGATGCTC  
TTTCAGCATCTTTAATGACCTCATGGGGTACATTCCACTGGTGAAGTATCTGCTCCCCAGACGG  
GGCCTCGCCTGAACACTCTCTGTGGATTGCTGATCTGATGGGGTACAGGATGTATGTCCGC  
GGAGTCGAACACAGAAAACCTGCTCTTCAACATCCTGGGCGGATGGGTGAAGGCTGCCGCTCT  
GGCCGACGGGGGATGCAGCGGCGGAGCTTACAGGCTCATTGTCTTCCCGATCTCGGAGTCAA  
ATTTTGGGCAAAGCACATGTGGAATTTATCGGGGTGGCCGGAGCCCTGGTCGCTTTTAAAAA  
GCAGCTCTTCACCTTCTCCCCAAGACGGAACGGATACCTCGTCGCCTACCAGGCCACTGTGGC  
TGCAGCTCTGCTCTTCTGCTCCTGGCCGATGCACTCATCTTCTGCCATTCCAAGAAAAAGTAT  
CTGGTCACCAGACATGCTGACGTGCTGGGGTTTGGCGCCTACATGAGCAAGTGCACCTGTGGC  
AGCTCCGACCTGTATCACATGTGGAACTTTATTTCTGGAATCTTTTGGGCCAAGCACATGTGG  
AATTTTAAGGCCGACGAGCTAAATTCGTGGCAGCCTGGACACTGAAAGCAGCTGCATGAGG  
ATCC (SEQ ID NO:106)

FIGURE 18F



HCV.4312(1P) (SEQ ID NO:107)

MGMQVQIQSLFLLLLWVPGSRGRLGVRATRKKAAAKTSERSQPRNLPGCSFSIFNDLMGYIPLVK  
YLLPRRGPRNLNLCGFADLMGYRMYVGGVEHRKLLFNILGGWVKAAALADGGCSGGAYRLIVFP  
DLGVKFWAKHMWNFIGVAGALVAFKKQLFTFSPRRNGYLVAYQATVAAALLFLLLADALIFCHS  
KKKYLVTNRHADVLGFGAYMSKCTCGSSDLYHMWNFISGIFWAKHMWNFKKAAAVLVGGVLA  
AFLLLADARVLSAFSLHSYILAGYGAGVWMNRLIAFANAAKFVAAWTLKAAA\*

GAATTCGCCGCCACCATGGAATGCAGGTGCAGATCCAAAGCCTGTTTCTGCTCCTCCTGTGG  
GTGCCCCGGCTCCAGAGGAAGGCTGGGCGTGAGAGCCACCCGGAAGAAGGCTGCCGCTAAAC  
AAGCGAGCGCTCCCAGCCCAGGAACCTGCCTGGATGCTCTTTCAGCATCTTTAATGACCTCAT  
GGGGTACATTCCACTGGTGAAGTATCTGCTCCCCAGACGGGGCCCTCGCCTGAACACTCTCTG  
TGGATTTGCTGATCTGATGGGGTACAGGATGTATGTCGGCGGAGTCGAACACAGAAAACTGCT  
CTTCAACATCCTGGGCGGATGGGTGAAGGCTGCCGCTCTGGCCGACGGGGGATGCAGCGGCG  
GAGCTTACAGGCTCATTGTCTTTCGGATCTCGGAGTCAAATTTTGGGCAAAGCACATGTGGA  
ATTTTCATCGGGGTGGCCGGAGCCCTGGTCGCTTTTAAAAAGCAGCTCTTCACCTTCTCCCCAA  
GACGGAACGGATACCTCGTCGCCTACCAGGCCACTGTGGCTGCAGCTCTGCTCTTCTGCTCC  
TGGCCGATGCACCTCATCTTCTGCCATTCCAAGAAAAAGTATCTGGTCACCAGACATGCTGACG  
TGCTGGGGTTTGGCGCTACATGAGCAAGTGCACCTGTGGCAGCTCCGACCTGTATCACATGT  
GGAACCTTTATTTCTGGAATCTTTTGGGCCAAGCACATGTGGAATTTTAAGAAAGCCGCTGCAG  
TCCTGGTGGGCGGCGTCTGGCAGCCGCTTTCCTGCTCCTGGCAGACGCCAGGGTGTGTCTG  
CCTTCAGCCTCCACTCCTACATCCTCGCAGGGTATGGCGCAGGCGTGTGGATGAATCGGCTGA  
TCGCCTTTGCCAATGCTGCAGCTAAATTCGTGGCAGCCTGGACACTGAAAGCAGCTGCATGAG  
GATCC (SEQ ID NO:108)

AOSL.K (SEQ ID NO:109)

MGMQVQIQSLFLLLLWVPGSRGHTLWKAGILYKAKFVAAWTLKAAAFLPDFFPSVKFLLSLGIH  
LYMDDVVLGVGLSRYVARLFLTRILTISTLPETTIVRRQAFTFSPTYKWLSLLVPFV

ATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGGTCCAGA  
GGACACACCCTGTGGAAGGCCGGAATCCTGTATAAGGCCAAGTTCGTGGCTGCCTGGACCCTG  
AAGGCTGCCGCTTTCCTGCCTAGCGATTTCTTTCCTAGCGTGAAGTTCCTGCTGTCCCTGGGAA  
TCCACCTGTATATGGATGACGTGGTGTGCTGGGAGTGGGACTGTCCAGGTACGTGGCTAGGCTGT  
TCCTGCTGACCAGAATCCTGACCATCTCCACCCTGCCAGAGACCACCGTGGTGAGGAGGCAGG  
CCTTCACCTTTAGCCCTACCTATAAGTGGCTGAGCCTGCTGGTGCCCTTTGTGTGA (SEQ ID NO:110)

HBV.1 (SEQ ID NO:111)

MGMQVQIQSLFLLLLWVPGSRGHTLWKAGILYKAKFVAAWTLKAAAFLPDFFPSVFLSLGIHL  
YMDDVVLGVGLSRYVARLFLTRILTISTLPETTIVRRQAFTFSPTYKWLSLLVPFVIPSSWAFTP  
ARVTGGVFKVGNFTGLYLPSDFFPSVTLWKAGILYKNVSIPWTHKLVDVFSQFSRSAICSVVRRAL  
MPLYACI

ATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGGTCCAGA  
GGACACACCCTGTGGAAGGCCGGAATCCTGTATAAGGCCAAGTTCGTGGCTGCCTGGACCCTG  
AAGGCTGCCGCTTTCCTGCCTAGCGATTTCTTTCCTAGCGTGTTCCTGCTGTCCCTGGGAATCC  
ACCTGTATATGGATGACGTGGTGTGCTGGGAGTGGGACTGTCCAGGTACGTGGCTAGGCTGTTCC  
TGCTGACCAGAATCCTGACCATCTCCACCCTGCCAGAGACCACCGTGGTGAGGAGGCAGGCCT  
TCACCTTTAGCCCTACCTATAAGTGGCTGAGCCTGCTGGTGCCCTTTGTGATCCCTATCCCTAG  
CTCCTGGGCTTTCACCCCAGCCAGGGTGACCGGAGGAGTGTTTAAGGTGGGAAACTTCACCGG  
CCTGTATCTGCCAGCGATTTCTTTCCTAGCGTGACCCTGTGGAAGGCCGGGATCCTGTACAA  
GAATGTGTCCATCCCTTGGACCCACAAGCTGGTGGTGGACTTTTCCAGTTCAGCAGATCCGC  
TATCTGCTCCGTGGTGAGGAGAGCTCTGATGCCACTGTATGCCTGTATCTGA (SEQ ID NO:112)

FIGURE 18G



HBV.2 (SEQ ID NO:113)

MGMQVQIQSLFLLLLWVPGSRGHTLWKAGILYKAKFVAAWTLKAAAFPSDFFPVSFNLLSLGIH  
LYMDDVVLGVLSRYVARLFLLTRILTISTLPETTIVRRQAFTFSPTYKGAAAWLSLLVPFVNPIIP  
SSWAFKTPARVTGGVFKVGNFTGLYNLPDFFPSVKTLWKAGILYKNVSIPWTHKGAALVVDQS  
FSRNSAICSVVRRALMPYACI

ATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGGTCCAGA  
GGACACACCCTGTGGAAGGCCGGAATCCTGTATAAGGCCAAGTTCGTGGCTGCCTGGACCCTG  
AAGGCTGCCGCTTTCCTGCCTAGCGATTTCTTTCCTAGCGTGAACCTCCTGCTGTCCCTGGGAA  
TCCACCTGTATATGGATGACGTGGTGTCTGGGAGTGGGACTGTCCAGGTACGTGGCTAGGCTGT  
TCTGTGTGACCAGAATCCTGACCATCTCCACCCTGCCAGAGACCACCGTGGTGAGGAGGCAGG  
CCTTACCTTTAGCCCTACCTATAAGGGAGCCGCTGCCTGGCTGAGCCTGCTGGTGCCCTTTGT  
GAATATCCCTATCCCTAGCTCCTGGGCTTTCAGACCCCAAGCCAGGGTGACCGGAGGAGTGTT  
TAAGGTGGGAAACTTCACCGGCCTGTATAACCTGCCAGCGATTTCTTTCCTAGCGTGAAGAC  
CCTGTGGAAGGCCGGAATCCTGTACAAGAATGTGTCCATCCCTTGGACCCACAAGGGAGCCG  
CTCTGGTGGTGGACTTTTCCAGTTCAGCAGAAATTCGGCTATCTGCTCCGTGGTGAGGAGAG  
CTCTGATGCCACTGTATGCCTGTATCTGA (SEQ ID NO:114)

PfCTL.1 (SEQ ID NO:115)

MQVQIQSLFLLLLWVPGSRGILSVSSFLFVNAAAQTNFKSLLRNLPSENERGYKAAALLACAGLAY  
KAAAAKFVAAWTLKAAAKAFMKAVCDEVNAAASFLFVEALFNATPYAGEPAPFKAAAKYKLA  
TSVLKAGVSENIFLNAAAAYFILVNLLIKAGLLGVVSTV

ATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGATCCAGA  
GGAATCCTGAGCGTGTCTCTTTCCTGTTTGTCAACGCCGCTGCACAGACCAATTTCAAGAGC  
CTCCTGAGGAACCTCCCTCCGAGAACGAAAGAGGCTACAAAGCCGCTGCACTGCTCGCCTGC  
GCTGGACTGGCCTATAAGAAAGCCGCTGCAGCCAAGTTCGTGGCCGCTTGGACACTGAAGGC  
CGCTGCAAAAGCCTTTATGAAGGCTGTCTGTGTGGAGGTCAATGCCGCTGCATCTTTCCTGTTT  
GTGGAGGCCCTCTTTAACGCTACTCCTTACGCAGGGGAACCAAGCCCTTCAAGGCCGCTGCA  
AAATATAAGCTGGCAACCAGCGTGTCTGAAGGCTGGCGTGTCCGAGAATATTTTTCTGAAAAAC  
GCCGCTGCATACTTCATCCTGGTGAATCTGCTCATTAAAGGCCGACTCCTGGGGGTGGTCTCT  
ACAGTGTGA (SEQ ID NO:116)

PfCTL.2 (SEQ ID NO:117)

MQVQIQSLFLLLLWVPGSRGFVEALFQEYNAAAKYLVIVFLINALACAGLAYKKFYFILVNLLKA  
ALFFIIFNKNAAAKFVAAWTLKAAAKFILVNLLIFHNFQDEENIGIYKLPYGRTNLKAAAVLLGGV  
GLVLNLIFFDLFLVKAVLAGLLGVV

ATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGATCCAGA  
GGATTCGTGGAGGCCCTGTTTCAGGAATACAACGCCGCTGCAAAGTATCTCGTCATCGTGTTT  
CTGATCAATGCTCTGGCATGCGCCGGCCTCGCTTACAAAAAGTTTTACTTCATTCTGGTCAACC  
TGCTCAAGGCCGCTCTGTTCTTTATCATTTTCAATAAAAACGCCGAGCTAAGTTTGTGGCCGC  
ATGGACCCTGAAGGCCGCTGCAAAATTCATCCTCGTGAATCTGCTCATTTTTTCAAACTTCCAA  
GACGAGGAAAATATCGGAATTTATAAGCTGCCCTACGGGAGGACAAACCTGAAAGCCGCTGC  
AGTCTGTCTCGCGGAGTGGGGCTGGTGCTCAATTTTCTGATCTTCTTTGATCTGTTCTCTGGTG  
AAGGCCGTCCTGGCCGGCCTGCTCGGAGTCGTGTGA (SEQ ID NO:118)

FIGURE 18H

PfCTL3 (SEQ ID NO:119)

MQVQIQSLFLLLLWVPGSRGVFLIFFDLFLNAAAPSDGKCNLYKAAAVTCGNGIQVRKLFHIFDGD  
NEIKAHVLSHNSYEKNYYGKQENWYSLKKILSVFFLANAAAKFIKSLFHIFKAAALYISFYFIKAKF  
VAAWTLKAAAKAAAYIPHQSSLKAAAGLIMVLSFL

ATGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCCGGATCCAGA  
GGAGTGTTCTGATCTTCTTTGACCTGTTCTGAAACGCCGCTGCACCCAGCGATGGCAAGTGC  
AATCTCTACAAGGCCGCTGCAGTGACCTGTGAAACGGGATTAGGTGAGGAACTCTTTTAC  
ATCTTCGACGGCGATAACGAGATCAAGGCCCATGTGCTGTCCACAATTCTTATGAAAAAAC  
TACTATGGAAAGCAAGAGAATTGGTACAGCCTGAAGAAAATTCTGTCCGTGTTCTTTCTCGCC  
AACGCCGCTGCAAAGTTTATCAAGTCTCTGTTCCATATTTTCAAGGCCGCTGCACTCTACATCA  
GCTTCTATTTTATTAAGCCAAATTTGTGGCCGCTTGACACTGAAGGCCGCTGCAAAGCCG  
CTGCATACTATATCCCTCACCAGAGCTCCCTGAAGGCCGCTGCAGGGCTGATCATGGTGCTCT  
CTTCTCTGTGA (SEQ ID NO:120)

PfCTL/HTL(N) (SEQ ID NO:121)

MQVQIQSLFLLLLWVPGSRGSSVFNVNNSIGLIMVLSFLGPGPGLYISFYFILVNLLIFHNGKIKN  
SEGPGPDPDSIQDSLKESRKLSPGPGLVLAGLLGVVSTVLLGGVGLVLPGPGLPSENERGYYPHQ  
SSLGPGPQTNFKSLRLNLGVSENIFLKGPGLFQDEENIGIYGPGLPYKTLNLGPGRHNWVNHAVPL  
GKFIKSLFHIFDGDNEIGPGLSKYKLTATSVLAGLLGPGLPYGKTLNLGPGRHNWVNHAVPL  
AMKLIGPGLMRKLAILSVSSFLFVEALFQYGPGLVTCGNGIQVRGPGLPMNYYGKQENWYSL  
KKGPGLPSDGKCNLYADSAWENVKNVIGPFMKAVCVEVGPGLKLSVFFLALFFIIFNKGPGLP  
HVLHNSYEKGPGPKYKLAGGIAGGLALLACAGLAYKFVVPGAATPYAGEPAPF

ATGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCCGGATCCAGA  
GGAAGTAGTGTTCAATGTTGTGAACCTCATCAATTGGTCTGATCATGGTGCTGAGCTTTCTCG  
GGCCAGGGCCAGGATTATATTTCTTTCTACTTCATCCTTGTC AACCTGTTAATATTCCACAT  
TAACGGCAAAATAATAAAGAACAGTGAAGGCCCTGGGCCTGGGCCTGACTCGATCCAGGATT  
CTCTAAAAGTAATCGAGGAAGCTCTCCGACCAAGGCCCTGGTGTACTCGCCGGGTGCTGGGA  
GTAGTTAGCACAGTGCTGTTAGGAGGCGTCGGCCTCGTCTTAGGACCTGGACCAGGTCTGCCG  
TCCGAAAACGAAAGAGGATACTACATACCTCACCAGAGCAGCCTCGGCCAGGCCCGGACA  
AACCAATTTCAAATCCCTCTTGCGAAATCTAGGAGTGAGCGAGAACATATTTCTTAAAGGACC  
CGTCCCGGCTTTTCAAGGACGAGGAGAAATATAGGTATTTACGGTCCAGGACCTGGAAAATACCT  
AGTGATCGTATTCCTAATTTTTTTTGTACCTATTTCTGGTGGGCCAGGTCCCGGAAAGTTCATT  
AAATCACTCTTCCACATTTTTTGTACGGAGATAACGAGATAGGACCCGGTCCCGGAAATCAA  
GTACAAACTAGCCACTTCAGTGCTGGCCGGCCTTCTAGGGCCGGGCCAGGGCTCCCTATGG  
AAAGACAAATCTTGCCCCGGTCCAGGACGGCACTGGGTGAATCATGCGGTTCCATTGG  
CCATGAAACTAATCGGGCCCGGTCCAGGCATGCGCAAACTTGCAATTCTAAGCGTAAGTTCAT  
TTCTGTTTCGTAGAGGCACTGTTTCAAGAATATGGCCAGGACCTGGCGTCACATGTGGGAATG  
GGATCCAGGTGAGAGGACCGGGACCTGGTATGAACCTATTACGGTAAACAGGAAAATTGGTAC  
TCCCTGAAAAAGGGTCCAGGCCCGGCCCTCAGATGGTAAGTGCAACCTGTATGCTGACTCA  
GCATGGGAGAACGTAAAAAATGTAATAGGCCCATTCATGAAGGCAGTTTGTGCGAAGTCGG  
ACCAGGCCAGGAAAAATACTTTCTGTCTTCTTCTAGCTCTCTTCTTCATCATCTTCAACAAG  
GGACCAGGGCCAGGTACGTGTTATCCATAACTCTTATGAAAAAGGGCCAGGACCTGGGAA  
ATACAAAATCGCAGGAGGGATCGCCGGCGGGCTAGCGCTCCTTGCCCTGCGCAGGCTTGGCTTA  
CAAATTCGTTGTACCAGGAGCTGCAACACCCTATGCAGGAGAACCTGCCCCATTTTGAAGATC  
TGC (SEQ ID NO:122)

FIGURE 18I



PF33 (SEQ ID NO:123)

MGMQVQIQSLFLLLLWVPGSRGFMKAVCDEVNVTGNGIQVRKGLIMVLSFLNAALFHIFDGDN  
EIKAAALLACAGLAYKKSFLFVEALFNAAPSDGKCNLYKAAQTNFKSLLRNLPSENERGYKAAGVS  
ENIFLNAAA YFILVNLLIKAAAILSVSSFLFVNTPYAGEPAPFKAAAKYKLATSVLKAAVFLIFFDL  
FLNYYIPHQSSLKAAGLLGNVSTVGAVLLGGVGLVNLACAGLAYKKAFIKSLFHIFKAAFYFIL  
VNLLKAFLIFFDLFLVKALFFIIFNKNYYGKQENWYSLKFVEALFQEYNAAAKFVAAWTLKAAAK  
ILSVFFLANAVLAGLLGNVNFQDEENIGIYKAAALYISFYFIKAFILVNLLIFHNAALPYGRTNLKAA  
HVLSHNSYEKNAAAKYLVIVFLI

GCCGCCACCATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCC  
GGATCCAGAGGATTTATGAAAGCTGTCTGTGTAGAGGTGAATGTAACATGCGGTAACGGAAT  
TCAGGTGAGAAAGGGACTCATCATGGTACTCAGCTTTCTGAACGCAGCCCTGTTCCACATCTT  
TGACGGAGACAATGAAATCAAAGCCGCATTGCTCGCCTGTGCCGACTAGCCTATAAAAAGA  
GTTTCCTTTTCGTTGAAGCACTATTTAACGCAGCACCCAGTGACGGTAAATGCAACCTATATA  
AAGCAGCTCAGACTAATTTCAAAGCCTGTAAAGAAATCTGCCCTCAGAGAATGAAAGGGGT  
TACAAAGCCGCGCGTGTCCGAGAATATTTTCTGAAGAACGCCGCTGCTTATTTTATACTC  
GTGAATCTACTCATAAAGGCAGCCGCAATCCTTTCAGTGTCCAGCTTTCTGTTTGTTAACACAC  
CATATGCGGGCGAGCCGGCTCCTTTCAAGGCTGCAGCAAAAATACAAGCTTGCCACATCAGTAT  
TGAAAGCAGCTGTGTTTTGATATTCTTTGATCTTTTTTAACTACTACATACCTCATCAGTCT  
AGTCTTAAAGCAGCCGGGCTACTGGGGAACGTCTCTACTGTGGGGGCCGCTTACTTGGAGGA  
GTTGGCCTCGTGTGTAACCTCGCGTGCAGGTCTGGCCTACAAAAAAGCGAAATTCATCAAG  
TCTCTGTTCCACATTTTTAAAGCCGCATTCTATTTCATACTAGTGAACCTTCTCAAAGCTTTCT  
GATCTTCTTCGATCTATTCTCGTAAAAGCGCTATTCTTCATTATCTTTAACAAAAATTATTAC  
GGCAAGCAAGAAAATTGGTACTCACTCAAGTTTGTAAGCTCTGTTCCAGGAATACAACGCC  
GCTGCTAAATTCGTTGCAGCTTGGACCTGAAAGCAGCTGCAAAGATCCTATCGGTCTTCTTTC  
TCGCTAATGCCGTATTAGCAGGACTTCTAGGCAACGTGAACTTTCAAGACGAAGAGAATATAG  
GCATCTACAAAGCCGAGCACTGTACATTTTCTTACTTTCATCAAGGCCTTCATACTGGTCAA  
CCTTCTGATATTTCATAATGCAGCACTGCCATATGGGAGAACCAACTTGAAAGCGGCCCCACGT  
GTTGAGCCACAACCTCTACGAGAAGAACGCCGCCGCGAAATATCTCGTCATTGTCTTCTCTGAT  
TTGA (SEQ ID NO:124)

TB.1 (SEQ ID NO:125)

MQVQIQSLFLLLLWVPGSRGRMSRVTTFTVKALVLLMLPVVNLMIQTAAAVVKALVLLMLPVGA  
GLMTAVYLVGAAAMALLRLPVKRMFAANLGVNSLYFGGICVGRPLVLPVAVNAAAACFVAAWT  
LKAAAKAAARLMIGTAAAGFVVALIPLVNMATYAAPLFVGAAMALLRLPLV

ATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCCGATCCAGAGGAAGG  
ATGAGCAGAGTGACCACATTCAGTCAAGGCCCTGGTGCTCCTGATGCTCCCCGTCGTGAAC  
CTGATGATCGGCACCGCTGCAGCCGCTCGTGAAAGCTCTCGTCCTGCTCATGCTCCCTGTGGGA  
GCAGGGCTGATGACAGCCGTGTACCTGGTCGGCGCTGCAGCCATGGCCCTCCTGCGGCTGCCA  
GTGAAGCGCATGTTTGCTGCAAATCTGGGAGTCAACTCCCTCTATTTGCGGGGCATTTGCGTG  
GGAAGGCTGCCCTCGTGCTGCCTGCTGTGAATGCAGCCGCTGCCAAATTTGTCGCCGCTTGG  
ACTCTGAAGGCAGCCGCTAAGGCCGCTGCAAGACTGATGATCGGGACCGCCGCTGCCGGCTT  
CGTGGTCGCCCTGATTCCCTGGTGAACGCCATGACATACGCAGCTCCTCTGTTTGTGGGAGC  
CGCTGCAGCCATGGCTCTCCTGCGGCTGCCACTGGTGTGA (SEQ ID NO:126)

FIGURE 18J





BCL A2 #90 (SEQ ID NO:127)

MQVQIQSLFLLLLWVPGSRGIMIGHLVGVNRLLQETELVNAKVAEIVHFLNAKVFGSLAFVNAYL  
SGANLNVGAAYLQLVFGIEVNAAAKFVAAWTLKAAAKAAAVVLGVVFGINSMPPPGTRVNAAA  
ATVGIMIGVNAKLCPVQLWV

ATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCCGGGTCCAGAGGAATT  
ATGATCGGCCATCTGGTGGGCGTCAACAGACTGCTGCAGGAAACCGAGCTGGTGAATGCCAA  
GGTGGCCGAAATTGTGCACTTTCTCAACGCAAAGGTGTTTGGTTCCTGGCTTTTGTCAATGCC  
TATCTGAGCGGCGCTAACCTCAACGTCGGAGCCGCTACCTCCAGCTGGTCTTCGGCATCGAG  
GTCAACGCTGCTGCAAAATTCGTGGCAGCTTGGACCCTCAAGGCTGCAGCAAAGGCTGCCGCC  
GTCGTGCTCGGAGTGGTGTTCGGGATCAACTCTATGCCACCTCCCGGGACTAGGGTCAATGCT  
GCCGCCGCAACAGTGGGAATCATGATTGGGGTGAATGCCAACTGTGCCAGTGCAACTGTG  
GGTGTGA (SEQ ID NO:128)

BCL A2 #88 (SEQ ID NO:129)

MQVQIQSLFLLLLWVPGSRGVVLGVVFGINAAAKFVAAWTLKAAAKVAEIVHFLNAYLSGANL  
NVGAAYLQLVFGIEVNIMIGHLVGVNRLLQETELVNAKVFGSLAFVNAKLCPVQLWVNAAAATV  
GIMIGVNSMPPPGTRV

ATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCCGGGTCCAGAGGAGTC  
GTGCTGGGAGTCGTCTTCGGCATTAAATGCCGCCGCTGCAAAGTTCGTGGCTGCCTGGACCCTG  
AAGGCCGCAGCTAAAGTGGCAGAGATCGTGCCTTTCTGAACGCCTACCTGAGCGGAGCAAA  
TCTGAACGTCGGCGCTGCCTATCTGCAGCTCGTGTGGAATTGAAGTGAACATCATGATTGG  
ACATCTGGTGGGCGTGAACAGGCTGCTCCAGGAACTGAGCTGGTCAACGCTAAAGTGTTCG  
GGTCTCTCGCCTTTGTGAACGCTAAGCTCTGCCCCGTCCAACCTCTGGGTCAATGCCGCAGCCG  
CTACAGTGGGGATCATGATCGGCGTGAACCTCCATGCCTCCACCAGGGACCAGAGTGTGA

(SEQ ID NO:130)

BCL A2 #63 (SEQ ID NO:131)

MQVQIQSLFLLLLWVPGSRGKLCPVQLWVNAAAATVGIMIGVNIMIGHLVGVNRLLQETELVNA  
KVAEIVHFLNAKVFGSLAFVNAYLSGANLNVGAAYLQLVFGIEVNAAAKFVAAWTLKAAAKAA  
AVVLGVVFGINSMPPPGTRV

ATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCCGGGTCCAGAGGAAAG  
CTCTGCCCCGTGCAACTGTGGGTCAACGCCGCCGCCGCAACCGTCGGCATTATGATCGGGGTG  
AACATCATGATCGGACACCTGGTCGGCGTGAACAGGCTGCTGCAGGAGACAGAACTGGTCAA  
TGCCAAGGTGGCTGAAATTGTCCATTTCTGAATGCCAAAGTGTTCCGGCTCTCTCGCTTTCTGTG  
AACGCTTATCTGAGCGGAGCTAACCTCAACGTGGGGGCCGCATACCTCCAGCTCGTCTTTGGG  
ATTGAGGTGAATGCCGCAGCTAAATTTGTGCTGCCTGGACCCTGAAGGCAGCAGCCAAGGCT  
GCCGCAGTGGTGTGGGAGTGGTGTGGAATCAATTCATGCCTCCACCAGGCACTAGAGTG  
TGAGGATCC (SEQ ID NO:132)

FIGURE 18K



Prostate 1 (SEQ ID NO:133)

LTFFWLDRSVKAAAVLVHPQWVLT VKAAALLQERGVAYIKAALLLSIALSVNPLVCNGVLQGVK  
AAIMYSAHDTTVKAAAF LTPKKLQCVNAMMNDQLMFLNAGLPSIPVHPV KAAALGTTTCYVGAAL  
LLWQPIPVNFLRPRSLQCVKAFLT LSVTWIGVNALLYSLVHNLGAATLMSAMTNL

ATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCGGGTCCAGAGGATTG  
ACATTTTTTTTGGCTGGATAGATCGGTAAAGGCTGCAGCCGTGCTTGTTTCATCCCCAGTGGGTCT  
TGACCGTAAAGGCTGCCGCGCTGCTACAAGAAAGAGGGGTGCGATACATCAAAGCTGCTCTC  
CTCTTGAGTATTGCGCTAAGTGTAACCCGCTAGTTTGTAATGGGGTGTTACAAGGTGTGAAA  
GCGGCGATTATGTACAGTGCCACGACACTACCGTAAAAGCAGCCGCTTTCCTGACCCCAAAA  
AAACTCCAATGCGTGAACGCAATGATGAATGATCAGCTGATGTTTTTAAACGCTGGCTTACCT  
TCTATACCGGTTTCATCCAGTCAAGGCCGCGGCTTGGGTACGACGTGTTATGTTGGAGCAGCG  
ATACTTCTTTGGCAGCCCATACAGTAAATTTTTTAAGACCTAGATCCTTACAATGCGTCAAAG  
CATTCTTACACTCTCAGTAACTTGGATCGGAGTCAATGCTCTGCTATATAGCCTCGTACACAA  
CTTGGGCGCGGCCACACTTATGAGTGCAATGACGAATTTAGCTAAGTTTCGTGGCGGCCTGGAC  
TCTAAAGGCCGCAGCA (SEQ ID NO:134)

HIV-1043 (SEQ ID NO:135)

MEKVYLAWVPAHKGIGGGPGPGQKQITKIQNFRVYYRGP GPGWFEVNTPLVKLWYQGP GPGYR  
KILRQRKIDRLIDGPGPGQHLLQLTVWGIKQLQGP GPGGEIYKRWII LGLNKIVRMYPGP GPGQGM  
VHQAI SPRTLNGP GPGIKQFINMWQEVGKAMYGP GPGWAGIKQEF GIPYNPQGP GPGKTA VQMA  
VFIHNFKRGP GPGSPAIFQSSMTKILEP GPGPGEVNIVTDSQYALGIIGP GPGHSNWRAMASDFNLPP  
GPGPGAETFYVDGAANRET KGP GPGGAVVIQD NSDIKVP GPGPGFRKYTAFTIPSINNE

ATGGAGAAGGTGTACCTGGCCTGGGTTCCAGCCCACAAAGGCATCGGGGGAGGGCCCCGGACC  
TGGGCAGAAACAGATCACCAAGATCCAGAACTTCCGGGTATACTACCGGGGACCTGGTCCAG  
GTTGGGAGTTTGTGAACACACCACCTTAGTAAAGCTCTGGTACCAGGGCCCCGGTCCCGGAT  
ACCGTAAAATCCTGAGGCAAAGAAAGATAGATCGCCTCATTGATGGCCCCGGGCCAGGCCAG  
CACCTTCTGCAGCTTACAGTGTGGGGAATTAAACAGCTGCAGGGGCCGGGCCCGGGGGGA  
AATTTATAAAAGGTGGATCATTCTGGGTCTGAACAAGATCGTCCGCATGTATGGCCCTGGACC  
CGGACAGGGGCAGATGGTCCACCAAGCAATCAGCCCTCGAACCTTGAATGGACCGGGGCCAG  
GAATCAAGCAATTCATTAACATGTGGCAAGAAGTTGGTAAGGCTATGTACGGTCCCGGCCCTG  
GATGGGCAGGGATAAAACAGGAGTTTGAATCCCTTACAATCCCCAGGGTCCTGGGCCAGGT  
AAAACGGCAGTGCAGATGGCCGTGTTCAATCATAATTTTAAGCGGGGCCCTGGACCTGGCAGC  
CCAGCTATATTTCAAAGTTCGATGACCAAAATCTTGGAGCCCGGCCAGGGCCGGGCGAAGT  
GAACATTGTACAGATTCTCAGTATGCCCTCGGCATCATAGGGCCCGGACCAGGGCATTCCAA  
TTGGCGGCCATGGCGTCTGACTTTAATCTACCTCCTGGGCCAGGCCCTGGCGCGGAACTTT  
CTATGTGGACGGCGCTGCAAACAGGGAGACTAAGGGACCCGGACCCGGCGGCGCTGTAGTCA  
TTCAGGACAACCTCAGACATCAAGGTGGTTCCTCGGTCCAGGCCCGGGTTCAGAAAGTATACCG  
CCTTCACTATTCCGTCCATCAACAATGAGTGA (SEQ ID NO:136)

FIGURE 18L



HIV-1043 PADRE (SEQ ID NO:137)

MEKVYLAWVPAHKGIGGGPGPGQKQITKIQNFRVYYRGP GPGWFEVNTPLVKLWYQGP GPGYR  
KILRQRKIDRLIDGPGPGQHLLQLTVWGIKQLQGP GPGGEIYKRWILGLNKIVRMYGP GPGQGQM  
VHQAI SPRTLNGP GPGIKQFINMWQEVGKAMYGP GPGWAGIKQEF GIPYNPQGPGPGKTA VQMA  
VFIHNFKRGP GPGSPAIFQSSMTKILEP GPGPGEVNIVTDSQYALGIIGP GPGHSNWRAMASDFNLPP  
GPGPGAETFYVDGAANRETKGPGPGGA VVIQDNSDIKVP GPGPGFRKYTAFTIPSINNEGPGPGA  
KFVAAWTLKAAA

ATGGAGAAGGTGTACCTGGCCTGGGTTCAGCCACAAAGGCATCGGGGGAGGGCCCCGGACC  
TGGGCAGAAACAGATCACCAAGATCCAGAACTTCCGGGTATACTACCGGGGACCTGGTCCAG  
GTTGGGAGTTTGTGAACACACCACCCTTAGTAAAGCTCTGGTACCAGGGCCCCGGTCCCCGAT  
ACCGTAAAATCCTGAGGCAAAGAAAGATAGATCGCCTCATTGATGGCCCCGGGCCAGGCCAG  
CACCTTCTGCAGCTTACAGTGTGGGGAATTAACAGCTGCAGGGGCCGGGCCCGGGGGGGA  
AATTTATAAAAGGTGGATCATTCTGGGTCTGAACAAGATCGTCCGCATGTATGGCCCTGGACC  
CGGACAGGGGCAGATGGTCCACCAAGCAATCAGCCCTCGAACCTTGAATGGACCGGGGCCAG  
GAATCAAGCAATTCATTAACATGTGGCAAGAAGTTGGTAAGGCTATGTACGGTCCCGGCCCTG  
GATGGGCAGGGATAAAACAGGAGTTTGAATCCCTTACAATCCCCAGGGTCTCTGGGCCAGGT  
AAAACGGCAGTGCAGATGGCCGTGTTCAATCATAATTTAAGCGGGGCCCTGGACCTGGCAGC  
CCAGCTATATTTCAAAGTTTCGATGACCAAAATCTTGGAGCCCGGCCAGGGCCGGGCGAAGT  
GAACATTGTACAGATTCTCAGTATGCCCTCGGCATCATAGGGCCCGGACCGGGCATTCCAA  
TTGGCGCGCCATGGCGTCTGACTTTAATCTACCTCCTGGGCCAGGCCCTGGCGCGGAAACTTT  
CTATGTGGACGGCGCTGCAAACAGGGAGACTAAGGGACCCGGACCCGGCGGCGCTGTAGTCA  
TTCAGGACAACCTCAGACATCAAGGTGGTTCCCGGTCCAGGCCCGGGTTCAGAAAGTATACCG  
CCTTCACTATTCCGTCCATCAACAATGAGGGCCCCGGCCAGGTGCCAAGTTCGTGGCTGCCT  
GGACCCTGAAGGCTGCCGCTTGA (SEQ ID NO:138)

HIV 75mer (SEQ ID NO:139)

EKVYLAWVPAHKGIGGGPGPGQGQM VHQAI SPRTLNGP GPGSPAIFQSSMTKILEP GPGPGFRKYTA  
FTIPSINNE

GAGAAGGTGTACCTGGCCTGGGTGCCTGCCACAAAGGAATCGGAGGACCTGGCCCTGGACA  
GGGACAGATGGTGCACAGGCCATCAGCCCTAGGACCCTGAACGGACCTGGACCTGGAAGCC  
CTGCCATCTTCCAGAGCAGCATGACCAAGATCCTGGAGCCCGGACCTGGACCTGGATTAGGA  
AGTACACCGCCTTCACCATCCCCAGCATCAACAACGAGTGA (SEQ ID NO:140)

FIGURE 18M



PHITL (SEQ ID NO:141)

MQVQIQSLFLLLLWVPGSRGRHNWVNHAVPLAMKLIGPGPGKCNLYADSAWENVKNGPGPGKS  
KYKLATSVLAGLLGPGPGQTNFKSLRLN LGVSEGPGPGSSVFN VVNSSIGLIMGPGPGVKNVIGPF  
MKA VCVGPGPGMNYYGKQENWYSLKKGPGPGGLAYKFVVPGAATPYGPGPGPDSIQDSLKESR  
KLNGPGPGLLIFHINGKIIKNSEGP GPGAGLLGNVSTVLLGGVGP GPGKYKIAGGIAGGLALLGPGP  
GMRKLAILSVSSFLFV

ATGGGAATGCAGGTGCAGATCCAGAGCCTGTTTCTGCTCCTCCTGTGGGTGCCCCGGATCCAGA  
GGAAGGCACAACTGGGTGAATCATGCTGTGCCCTGGCTATGAAGCTGATCGGCCCTGGACC  
AGGGAAATGCAACCTCTACGCAGACAGCGCCTGGGAGAACGTCAAGAATGGCCCCGGACCTG  
GGAAATCCAAGTATAAGCTCGCTACCTCTGTGCTGGCAGGCCTGCTCGGACCAGGCCCGGAC  
AGACAAATTTCAAAGCCTGCTCAGAAACCTGGGAGTGTCCGAGGGGCCTGGCCCAGGATCT  
AGCGTCTTTAATGTGGTCAACTCCTCTATTGGGCTCATCATGGGACCCGGACCTGGGGTGAAA  
AATGTGATTGGCCCATTCATGAAGGCCGTGTGTGTGCGAAGGACCCGGGCCTGGCATGAACTAC  
TATGGAAAGCAAGAAAATTGGTACAGCCTGAAGAAAGGCCCTGGGCCAGGCGGACTGGCTTA  
CAAGTTTGTGGTCCCAGGGGCAGCCACTCCCTATGGGCCTGGGCCAGGCCCCGATTCCATCCA  
GGACTCTCTCAAAGAGAGCCGGAAGTGAACGGACCCGGGCCTGGACTGCTCATTTTCCACAT  
CAATGGCAAAATTATCAAGAACAGCGAGGGACCTGGGCCAGGCGCCGACTGCTGGGGAACG  
TGTCACCGTCCTGCTCGGCGGAGTGGGGCCCCGCCCTGGGAAGTACAAGATCGCTGGAGGG  
ATCGCAGGCGGACTGGCCCTCCTGGGCCAGGACCAGGGATGCGCAAAGTGGCTATTCTCTCT  
GTCTCCAGCTTTCTGTTTGTGTGA (SEQ ID NO:142)

FIGURE 18N



Protein	Sequence(SEQ ID NOS:143-340)	Restriction
HIV gag 386	VLAEAMSQV	HLA-A2
HIV gag 271	MTNNPPIPV	HLA-A2
HIV pol 774	MASDFNLPPV	HLA-A2
HIV pol 448	KLVGKLNWA	HLA-A2
HIV pol 163	LVGPTPVNI	HLA-A2
HIV pol 498	ILKEPVHGV	HLA-A2
HIV pol 879	KAACWWAGI	HLA-A2
HIV pol 132	KMIGGIGGFI	HLA-A2
HIV pol 772	RAMASDFNL	HLA-A2
HIV pol 183	TLNFPISPI	HLA-A2
HIV env 134	KLTPLCVTL	HLA-A2
HIV env 651	LLQLTVWGI	HLA-A2
HIV env 163	SLLNATDIAV	HLA-A2
HIV nef 221	LTFGWCFKL	HLA-A2
HIV vpr 59	AIIRILQQL	HLA-A2
HIV vpr 62	RILQQLLFI	HLA-A2
HIV pol 929	QMAVFIHNFK	HLA-A3
HIV pol 722	KVYLAWVPAHK	HLA-A3
HIV pol 971	KIQNFRVYYR	HLA-A3
HIV pol 347	AIFQSSMTK	HLA-A3
HIV pol 98	VTIKIGGQLK	HLA-A3
HIV env 61	TTLFCASDAK	HLA-A3
HIV env 47	VTVYYGVPVWK	HLA-A3
HIV nef 100	QVPLRPMTYK	HLA-A3
HIV vif 7	VMIVWQVDR	HLA-A3
HIV gag 162	QMVHQAISPR	HLA-A3
HIV gag 545	YPLASLRS LF	HLA-B7
HIV gag 237	HPVHAGPIA	HLA-B7
HIV pol 186	FPISPIETV	HLA-B7
HIV pol 893	IPYNPQSQGVV	HLA-B7
HIV env 259	IPIHYCAPA	HLA-B7
HIV env 250	CPKVSFEPI	HLA-B7
HIV nef 94	FPVRPQVPL	HLA-B7
HIV rev 75	VPLQLPPL	HLA-B7
HIV pol 684	EVNIVTDSQY	HLA-A1
HIV gag 317	FRDYVDRFY	HLA-A1
HIV pol 368	VITYQYMDDL Y	HLA-A1
HIV pol 295	VTVLDVGDAY	HLA-A1
HIV pol 533	IYQEPFKNL	HLA-A24
HIV pol 244	PYNTPVFAI	HLA-A24
HIV pol 530	TYQIQEPF	HLA-A24
HIV pol 597	YWQATWIPEW	HLA-A24
HIV env 681	IWGCSGKLI	HLA-A24
HIV env 671	RYLKDQQLL	HLA-A24

FIGURE 19A



Protein	Sequence	Restriction
HIV env 55	VWKEATTTLF	HLA-A24
HIV vpr 46	IYETYGDTW	HLA-A24
HIV vpr 14	PYNEWTLEL	HLA-A24
HIV gag 298	KRWIILGLNKIVRMV	HLA-DR
HIV pol 596	WEFVNTPLVLKLYWYQ	HLA-DR
HIV pol 956	QKQITKIQNFRVYYR	HLA-DR
HIV pol 712	KVYLAWVPAHKGIGG	HLA-DR
HIV gag 294	GEIYKRWIILGLNKI	HLA-DR
HIV pol 711	EKVYLAWVPAHKGIG	HLA-DR
HIV env 729	QHLLQLTVWGKQLQ	HLA-DR
HIV gag 171	QGQMVHQAI SPRTL N	HLA-DR
HIV pol 335	SPAIFQSSMTKILEP	HLA-DR
HIV env 566	IKQFINMWQEVGKAMY	HLA-DR
HIV pol 303	FRKYTAFTIPSINNE	HLA-DR
HIV pol 758	HSNWRAMASDFNLPP	HLA-DR
HIV pol 915	KTAVQMAVFIHNFKR	HLA-DR
HIV vpu 31	YRKILRQRKIDRLID	HLA-DR3
HIV pol 874	WAGIKQEF GIPYNPQ	HLA-DR3
HIV pol 674	EVNIVTDSQYALGII	HLA-DR3
HIV pol 619	AETFYVDGAANRETK	HLA-DR3
HIV pol 989	GAVVIQDN SDIKVVP	HLA-DR3
HCV NS4 1812	LLFNILGGWV	HLA-A2
HCV NS1/E2 728	FLLLADARV	HLA-A2
HCV NS4 1590	YLVAYQATV	HLA-A2
HCV NS5 2611	RLIVFPDLGV	HLA-A2
HCV CORE 132	DLMGYIPLV	HLA-A2
HCV NS4 1920	WMNRLIAFA	HLA-A2
HCV NS4 1666	VLVGGVLAA	HLA-A2
HCV NS4 1769	HMWNFISGI	HLA-A2
HCV NS4 1851	ILAGYGAGV	HLA-A2
HCV CORE 35	YLLPRRGPR L	HLA-A2
HCV NS1/E2 726	LLFLLLADA	HLA-A2
HCV LORF 1131	YLVTRHADV	HLA-A2
HCV CORE 51	KTSE RSQPR	HLA-A3
HCV CORE 43	RLGVRATRK	HLA-A3
HCV ENV1 290	QLFTFSPRR	HLA-A3
HCV NS1/E2 632	RMVVG GVEHR	HLA-A3
HCV NS3 1396	LIFCHSKKK	HLA-A3
HCV NS4 1863	GVAGALVAFK	HLA-A3
HCV NS4 1864	VAGALVAFK	HLA-A3
HCV NS3 1262	LGFGAYMSK	HLA-A3
HCV Core 169	LPGCSFSIF	HLA-B7
HCV NS5 2922	LSAFSLHSY	HLA-A1
HCV NS3 1128	CTCGSSDLY	HLA-A1
HCV NS5 2180	LTDPSHITA	HLA-A1

FIGURE 19B



Protein	Sequence	Restriction
HCV Core 126	LTCGFADLMGY	HLA-A1
HCV NS3 1305	LADGGCSGGAY	HLA-A1
HCV NS4 1765	FWAKHMWNF	HLA-A24
HCV NS5 2875	RMILMTHFF	HLA-A24
HCV NS5 2639	VMGSSYGF	HLA-A24
HCV NS4 1765	FWAKHMWNFI	HLA-A24
P. falciparum SSP2-230	FMKAVCVEV	HLA-A2
P. falciparum EXP1-83	GLLGVVSTV	HLA-A2
P. falciparum CSP-7	ILSVSSFLFV	HLA-A2
P. falciparum LSA1-94	QTNFKSLLR	HLA-A3
P. falciparum LSA1-105	GVSENIFLK	HLA-A3
P. falciparum SSP2-522	LLACAGLAYK	HLA-A3
P. falciparum SSP2-539	TPYAGEPAPF	HLA-B7
P. falciparum LSA1-1663	LPSENERGY	HLA-A1
P. falciparum EXP1-73	KYKLATSVL	HLA-A24
P. falciparum CSP-12	SFLFVEALF	HLA-A24
P. falciparum LSA1-10	YFILVNLLI	HLA-A24
P. falciparum SSP2-14	FLIFFDLFLV	HLA-A2
P. falciparum EXP1-80	VLAGLLGVV	HLA-A2
P. falciparum EXP1-91	VLLGGVGLVL	HLA-A2
P. falciparum SSP2-523	LACAGLAYK	HLA-A3
P. falciparum EXP1-10	ALFFIIFNK	HLA-A3
P. falciparum LSA1-11	FILVNLLIFH	HLA-A3
P. falciparum SSP2-126	LPYGRTNL	HLA-B7
P. falciparum CSP-15	FVEALFQEY	HLA-A1
P. falciparum LSA1-1794	FQDEENIGIY	HLA-A1
P. falciparum LSA1-9	FYFILVNLL	HLA-A24
P. falciparum SSP2-8	KYLVIVFLI	HLA-A24
P. falciparum CSP-394	GLIMVLSFL	HLA-A2
P. falciparum EXP1-2	KILSVFFLA	HLA-A2
P. falciparum CSP-344	VTCGNGIQVR	HLA-A3
P. falciparum LSA1-59	HVLSHNSYEK	HLA-A3
P. falciparum SSP2-207	PSDGKCNLY	HLA-A1
P. falciparum LSA1-1671	YYIPHQSSL	HLA-A24
P. falciparum LSA1-1876	KFIKSLFHIF	HLA-A24
P. falciparum SSP2-13	VFLIFFDLFL	HLA-A24
P. falciparum LSA1-1881	LFHIFDGDNEI	HLA-A24
P. falciparum CSP-55	YYGKQENWYSL	HLA-A24
P. falciparum LSA1-5	LYISFYFI	HLA-A24
P. falciparum CSP-2	MRKLAILSVSSFLFV	HLA-DR
P. falciparum CSP-53	MNYYGKQENWYSLKK	HLA-DR
P. falciparum CSP-375	SSVFNVVNSSIGLIM	HLA-DR
P. falciparum SSP2-61	RHNWVNHAVPLAMKLI	HLA-DR
P. falciparum SSP2-165	PDSIQDSLKESRKLN	HLA-DR3
P. falciparum SSP2-211	KCNLYADSAWENVKN	HLA-DR3

FIGURE 19C



Protein	Sequence	Restriction
P. falciparum SSP2-223	VKNVIGPFMKAVCVE	HLA-DR
P. falciparum SSP2-509	KYKIAGGIAGGLALL	HLA-DR
P. falciparum SSP2-527	GLAYKFVVPGAATPY	HLA-DR
P. falciparum EXP1-71	KSKYKLATSVLAGLL	HLA-DR
P. falciparum EXP1-82	AGLLGNVSTVLLGGV	HLA-DR
P. falciparum LSA1-16	LLIFHINGKIIKNS	HLA-DR
P. falciparum LSA1-94	QTNFKSLLRN LGVSE	HLA-DR
HBV core 18	FLPSDFFPSV	HLA-A2
HBV env 183	FLLTRILTI	HLA-A2
HBV env 335	WLSLLVPFV	HLA-A2
HBV pol 455	GLSRYVARL	HLA-A2
HBV pol 538	YMDDVVLGV	HLA-A2/A1
HBV pol 773	ILRGTSFVYV	HLA-A2
HBV pol 562	FLLSLGIHL	HLA-A2
HBV pol 642	ALMPYACI	HLA-A2
HBV env 338	GLSPTVWLSV	HLA-A2
HBV core 141	STLPETTVVRR	HLA-A3
HBV pol 149	HTLWKAGILYK	HLA-A3/A1
HBV pol 150	TLWKAGILYK	HLA-A3
HBV pol 388	LVVDFSQFSR	HLA-A3
HBV pol 47	NVSIPWTHK	HLA-A3
HBV pol 531	SAICSVVRR	HLA-A3
HBV pol 629	KVGNFTGLY	HLA-A3/A1
HBV pol 665	QAFTFSPTYK	HLA-A3
HBV core 19	LPSDFFPSV	HLA-B7
HBV env 313	IPIPSSWAF	HLA-B7
HBV pol 354	TPARVTGGVF	HLA-B7
TB	RMSRVTTFTV	HLA-A2
TB	ALVLLMLPVV	HLA-A2
TB	LMIGTAAAVV	HLA-A2
TB	ALVLLMLPV	HLA-A2
TB	GLMTAVYLV	HLA-A2
TB	MALLRLPV	HLA-A2
TB	RMFAANLGV	HLA-A2
TB	SLYFGGICV	HLA-A2
TB	RLPLVLPV	HLA-A2
TB	RLMIGTAAA	HLA-A2
TB	FVVALIPLV	HLA-A2
TB	MTYAAPLFV	HLA-A2
TB	AMALLRLPLV	HLA-A2
p53 139	KLCPVQLWV	HLA-A2
CEA 687	ATVGMIGV	HLA-A2
CEA 691	IMIGHLVGV	HLA-A2
Her2/neu 689	RLLQETELV	HLA-A2
MAGE3 112	KVAEIVHFL	HLA-A2

FIGURE 19D





Protein	Sequence	Restriction
Her2/neu 369	KVFGSLAFV	HLA-A2
CEA 605	YLSGANLNV	HLA-A2
MAGE2 157	YLQLVFGIEV	HLA-A2
Her2/neu 665	VVLGVVFGI	HLA-A2
p53 149	SMPPPGTRV	HLA-A2
PAP.21.T2	LTFFWLDRSV	HLA-A2
PAP.112	TLMSAMTNL	HLA-A2
PAP.284	IMYSAHDTTV	HLA-A2
PSM.288.V10	GLPSIPVHPV	HLA-A2
PSM.441	LLQERGVAYI	HLA-A2
PSM.469L2	LLYSLVHNL	HLA-A2
PSM.663	MMNDQLMFL	HLA-A2
PSA.3.V11	FLTLSVTWIGV	HLA-A2
PSA.143.V8	ALGTTCYV	HLA-A2
PSA.161	FLTPKKLQCV	HLA-A2
HuK2.4.L2	LLLSIALSV	HLA-A2
HuK2.53.V11	VLVHPQWVLTV	HLA-A2
HuK2.165	FLRPRSLQCV	HLA-A2
HuK2.216.V11	PLVCNGVLQGV	HLA-A2

FIGURE 19E